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Database length: -79123438
Search time (sec): 491.860000
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-Q-/cgn2_1/USPTO_spool/US9510332/runat_06032001_093637_13621/app_query.fasta_1.359
-Q-/cgn2_1/USPTO_spool/US9510332/runat_06032001_093637_13621/app_query.fasta_1.359
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-MAXLEN=20000000000 -USER=US09510332_@CGN1_1_2364 -NCPU=6
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                            alignment_scores:
Quality: 1165.00
Ratio: 5.155
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US-09-510-332-1 x AQ308694
AQ308694 742 bp DNA CITBI-E1-2530B8.TF CITBI-E1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
seq primer: M13-21
Class: BAC ends.
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Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
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Use of a random human BAC End Sequence Database for Sequence-Ready
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                          AQ308694 from: 1 to: 742
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CalTech Human BAC Library D"
175 c 144 g 247 t
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LOCUS A0316000
                                                                                                                                                                                                                                                                            seq_name: gb_gss4:AQ316999
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Map Building
Unpublished (1998)
Contact: Shaying Zhao, William Nierman,
Contact: Shaying Zhao, William Nierman,
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Rockville, MD
  end
    Clones are availabe from Research Genetics (info@resgen.com).
                           9712 Medical Center Dr.,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                 Berry, K., 6
Venter, J.C.
                                                                                                                                                                                                                  AQ316999
                 Email: hbe@tigr.org
                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 650)
                                                                                                                                                                                                                                     AQ316999 650 k
CITBI-E1-2530B7.TF
                                                                                                         Use of a random human BAC
                                                                                                                        Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S.,
Berry,K., Granger,D., Suh,E., Wible,C., Shiz
                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                         AQ316999.1 GI:4040265
search page:
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F CITBI-El Homo sapiens genomic
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                                                                                                        Sequence
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                                                                           Mark
                                                                                                                       s,S., Linher,K., Golden,K.
Shizuya,H., Simon,M. and
                                                                                                      for
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Ratio: 5.120
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                             AAATGAGAAACACAGTGGCCGGCAGCAGGGTTCCTGGCAGGGGTGCACCC
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                                                                                                                                                     CCTTTTTGCTGTTTTGCTCTTGATTTTCTCTCTGGGGAGGCACACCCGGC
                                                                                                                                                                eLeuPheAlaValLeuLeuLlePheSerLeuGlyArgHisThrArgG
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CalTech Human BAC Library D*
a 152 c . 125 g 224 t
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                                                                                                                                      3 AAGCTGGTCCCATGGATGATCCTGGGGTCTCTGCTATATGTATCTATGAT
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rgLysPhePheSerGlnAsnAlaThrIleGlnLysGluAspThrLeuAla 173
                                                                             eCysValPheHisSerLysTyrAlaGlyPheMetValProTyrPheLeuA 157
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CITBI-E1-2516A7.TF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html. Seg primer: M13-21 Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Mark Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1998)
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Clones are available from Research Genetics (info@resgen.com). BAC
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2 Medical Center Dr., Rockville,
301 838 0200
301 838 0208
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2 77 c 69 g 88 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU-Merck EST project 1997
unpublished (1997)
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zu05e04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730974
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                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -41m13 fwd. ET from Amersham High quality sequence stop: 413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
                140
           /organism="Homo sapiens"
/db_xref="GDB:5927764"
                                                                                                                                                                                                                      /clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:730974"
                                                                                                                                                                                        /lab_host="DH10B"
                                                                                                                                                                                                       'sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MO 63108
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alignment\_scores: Quality:

406.00

Length:

83

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FEATURES
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ORGANISM
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS A0616191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio: 4.892
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-510-332-1 x AA416581/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCTTTCTTGTCTGGCAGTTTCTAGAATTTTTCTGCAGTTGTTCATCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gb_gss9:AQ616191
                                                                                                                                                                                       Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Clones availability, please contact Pleter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                         http://www.htsc.washington.edu
Plate: 724 row: K column: 10
Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 498)

Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A0616191 498 bp DNA GSS 15-JUN-1999
HS_5148_A2_F05_SP6E RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=724 Col=10 Row=K, DNA sequence.
                                                                                                                                                                                                                                                                                                          401 Queen Anne Avenué North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                          High Throughput Sequencing Center University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence-tagged connectors: A sequence approach to mapping scanning the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ616191.1 GI:5077555
                                                                                        quality sequence stop: 498 
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9666"
/clone="plate=724 Col=10 Row=K"
/clone_lib="RPCI-11 Human Male BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps: 0
Percent Identity: 97.590
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                                                                                  REFERENCE
AUTHORS
TITLE
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SOURCE
ORGANISM
                                                                                                                                                                                                                             ACCESSION
VERSION
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                                                                                                                                                                                                                                                                                                                                                                                            472
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seq_documentation_block:
LOCUS AL037695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-510-332-1 x AQ616191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   422 GCTTCTGGGAAGCGGTCTGGCCTCTGTGAGCATTGCATCTGTGTGTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 roLeuPheIleTrpLeuLysMetArgIleSer.LysLeuValProTrpMe 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 CATAGCGATGTCTACAATTGGTCTGCAGATGGTAGTAATGGTACAAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 GAATTGATCAAACATAGAAAGCTAATGCCAATTCAAATCCTCTTAATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 TTTTCTCTGTGTTCTTTCCACTCCTTTACGTCAAAATAATCTATGGTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 sLeuAlaValSerArgIlePheLeuGlnLeuPheIlePheTyrValAsnV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTAGATTACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerLysTyrAla 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tIleLeuGlySer...LeuLeuTyrValSerMetIleCysVal.PheHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTGTTTTCTTTGGTGAAATTCAGGA...TCCAAAGGTAATACCTTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aThrTrpLeuGlyValPheTyrCysAlaLysValAlaSerValArgHisP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCAATGACGTTCCTTTGGATGTTTTTTAACTCTATCAGCCTATGGGTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AlaAsnCysAlaIleLeuLeuPheIleAsnGluLeuGluLeuTrpLeuAl 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             allleValllePhePhe......IleGluPheIleMetCysSer 79
                                                                                                                                                                                                                                                                                                                                                  AL037695 554 bp mRNA EST DKFZp56400672_rl 564 (synonym: hfbr2) Homo DKFZp56400672 5', mRNA sequence.
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
                                                                   Contact: Blum H
                                                                                   Unpublished (1999)
On Jul 7, 1999 this
                                                                                                                               Blum, H., Bauersachs, S., Mewes, H.W., EST (Blum, et al.)
                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                        EST.
                                                                                                                                                                                                                                                                                                             AL037695.3 GI:5928268
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                                                                                                                                                                             (bases 1 to 554)
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6
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104 c 112 g 155 t 7 others
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2.402
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                                                                                                                                                                                                Chordata;
Primates;
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Gaps:
Percent Identity:
                                                                                   sequence version replaced g1:5866546
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                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                      Gassenhuber,J.
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5
39.344
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                                                                                                                                                      and Wiemann, S
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BASE COUNT
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seq_documentation_block:
LOCUS AZ396344
                                                           seq_name: gb_gss20:AZ396344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-510-332-1 x AL037695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
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                                                                                                                                                    138
                                                                                                                                                                                                                                                                                                   105 laLysValAlaSerValArgHisProLeuPheIleTrpLeuLysMetArg 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 TCTCCTCAACTGACCAAATTGTCACTGCTCTGGCATTCTCCAGAATTGGT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 LeuGlnLeuPheIlePheTyrValAsnValIleValIlePhePheIleGl 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 etAlaProLeuAspLeuLeuLeuSerCysLeuAlaValSerArgIlePhe 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 nGlyIleIleValValAsnGlyIleAspLeuIleLysHisArgLysM 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ű
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uPheIleMet.CysSerAlaAsnCysAlaIle.....Leu.LeuPheIl 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTACTTTGATCATATTATTACATTGGTATGCAACTGTGTTTAATTCAGCT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGCTTCATAGCTCTAGTTAATGTCAATGACTGGGTTAAGACACAAAAGA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IleTyrPheLeuLeuAlaValIleGlnPheLeuLeuGlyIlePheThrAs
                                                                                                                                                                                                                                                                                 TCAAGATTGCCAATTTCTCCAATTTTATTTTTCTCCACCTAAAGAAGAGA
                                                                                                                                                                                                                                                                                                                                                                     eAsnGluLeuGluLeuTrpLeuAlaThrTrpLeuGlyValPheTyrCysA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTATATAGTTTAGAAGTAAGAATTGTTCCTTCTAATGTCTCGGCAATAAT 254
                                                                                                                                                    rMetIleCys 141
                                                                                                                                                                                             ATTAAGAGTGTTCTTGTGATACTGTTGGGGTCCTTGGTATTT....
                                                                                                                                                                                                                                      IleSerLysLeuValProTrpMetIleLeuGlySerLeuLeuTyrValSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by LMU (Ludwig Maximilians University,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone (DKF2p56400672) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s1 sequence also available.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Munich/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Berlin-Charlottenburg, GERMANY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="DKFZp5640672"
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/dev_stage="fetal"
/lab_host="xl-2blue"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"
96 c 108 g 196 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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  710 bp
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Percent Identity: 35.507
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      GSS
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      03-OCT-2000
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SOURCE
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                                           alignment_block:
US-09-510-332-1 x AZ396344/rev
                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                alignment_scores:
Align seg 1/1 to reverse of: AZ396344
                                                                                                               Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ddunn@genetics.utah.
Insert Length: 10000 Std
Plate: 0160 row: C column
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B. University of Utah University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly, Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ396344.1 GI:10511416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 801 585 5606 Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 710
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                                                                                                                                       Ratio:
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                                                                                                                                                                                                                                                                  was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gil4732114|gb\AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XIIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                 170.50
1.705
62.893
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/clone="UUGC1M0160C21"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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Genome Center
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                                                                                                                      Percent
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IleIleTyrPheLeuLeuAlaValIleGlnPheLeuLeuGlyIlePheTh 23

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SOURCE
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LOCUS AZ416308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 TCAG...CTCGCCTGCTTCCAGCAGGATGAAAGACCCACTGAGCCACAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGATGCTTCTAGTTGTTCTTCTCTCTCCTGCATCTGCACTGCCCTTGTT
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                     Email: ddunn@genetlcs.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0191 row: D column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 656)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ416308 656 bp DNA GSS 03-OCT-2000 1M0191D04R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0191D04 R, DNA sequence.
AZ416308
                                                                                                                                                                                             Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
       High quality sequence stop: 656
                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                         plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                       Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 LeuIlePheLeuPheAlaValLeuLeuIlePheSerLeuGlyArgH1
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                                                                                                                     AsnAlaLysLysPheLeuLeuHisSerLysCysCysGln 299
                                                                                                                                                                                                                                                                                                                                                                          sIleArgArgPheIlePheLeuPhePheIleLeuValIleGlyIleTyrP 270
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                                                              TGCTCTGTAATGATACTGCAACTATTAAAGTGCTGTGAG 249
                                                                                                                                                                                   CCGGCTGCCACTCACTTATCCTAATTCTAGCAAACAGTCGGCTGAAGCAG
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/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/50 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/clone="UUGC1M0191D04"
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/strain="C57BL/6J"
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                                             147
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                                                                                                                                     131 uGlySerLeuLeu...TyrValSerMetIleCysValPheHisSerLys. 146
438
                                        TyralaGlyPheMetValProTyrPheLeuArgLysPhePheSerGlnAs 163
                                                                                                                                                                                          TTTCTTTGGTTGAAATTCAGGATCCCANAGTTAATACCTTGGCT.GTTCT
TACGCTANAAATGTGGAAGAGGATGCCCTCAGA.....AA
                                                                                             AQ711250 538 bp DNA GSS 13-JUL-1999
HS_5349_B2_H04_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate-925 Col-8 Row-P, DNA sequence.
AQ711250
AQ711250.1 GI:5460566
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.htsc.washington.edu
plate: 925 row: P column: 8
Seq primer: T7
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University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Mahairas GG, Wallace JC, High Throughput Sequencing Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u. washington.edu
Clones are derived from the human BAC library RPCI-11. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
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97 c 111 g 156 t 9 others
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/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306
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                                                                                                                                                                 Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
plate: 399 row: P column: 19
                                                                                                                                                                                                                                                                                                                                                               Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-399P19.TJ
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 644)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Shaying Zhao
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                    /organism="Mus musculus"
/strain="C57BL/6J"
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Rockville,
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K., Krol,M.,
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                euLysPheHisIleArgArgPheIlePheLeuPhePheIleLeuValIle 266
                                                                                                                                                                                                                                                                                                                                                                                  ....IleLeuTyrPheSerHisCysMetIleLysValPheLeuSerSerL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                           ACAGAAGCACACATAAAAGCTATGAAAACTATGATGTCATTCCTTTTGTT 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATGATAGCTAAT.....AATTTTATCTACAAATGGACAAAAT 100
                                                                 gb_est66:BE033430
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/clone_lib="RPCI-23"
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alignment_block:
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Percent Similarity:
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
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                            95 uAlaThrTrpLeuGlyValPheTyrCysAlaLysValAlaSerValArgH 112
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TTCTACTTTCCTTCCTTTTTTCTTT...
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                                                                 AlaIleLeuLeuPheIleAsnGluLeuGluLeuTrp.....Le 95
                                                                                                                                      rgLysMetAlaProLeuAspLeuLeuSeuCysLeuAlaVal.SerAr 55
                                                                                                                                                                                                                                                                                                                                                                                        eThrAsnGlyIleIleValValValAsnGlyIleAspLeuIleLysHisA 39
                                                                                                                                                                      he.....lleGluPheIleMetCysSerAlaAsnCys 82
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eudicotyledons; core eudicots; Caryophyllidae;
Caryophyllales; Alzoaceae; Mesembryanthemum.

1 (bases 1 to 1176)
Bohnert, H. J., Borchert, C., Brazille, S., Brooks, J., Eaton, M., Ferrea, H., Kawasaki, S., McCollough, A., Michalowski, C.B., Palacio, C.,
Scara, G., Wheeler, M. and Zepeda, G.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bio Sciences West room 513, Tel: 520-621-7982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
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BE033430
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open reading frame exists.
Location/Qualifiers
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/note="grown in hydroponics,
Hoagland's); 6 h stress"
1 324 c 65 g 658 t
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/clone_lib="ME"
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KEYWORDS
SOURCE
ORGANISM
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LOCUS B17827
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TITLE
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B17827
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               9712
Tel:
                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 466)
Adams, M.D., Kelley, J.M., Rounsley, S.R. and Venter, J.C.
Use of a BAC End Sequence Database for Sequence-Ready Map Building Unpublished (1997)
Other_GSSs: 347L19.TVB
                                                                       Contact: Mark Adams
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                       B17827.1 GI:2125576
Institute for Genomic Research
Medical Center Dr., Rockville,
301 838 0200
301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1140
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BASE COUNT
ORIGIN
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US-09-510-332-1 x B17827
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KEYWORDS
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LOCUS BE734359
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TCTTAGGACACAGCAGAGCAAACTTGTACTCCTGCCTTTGCCAAACTGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com).
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1544)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
                                                                                                                                                                       BE734359 1544 bp
601565606F1 NIH_MGC_21
                                                                                                                                        mRNA sequence.
BE734359
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CalTech Human BAC Library Al"
108 c 82 g 141 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="A-347L19"
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1.967
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AUTHORS

122 les ::	105 aLys : 917 TCTC	89 Asn ::: 967 GGT	72 hei   : 999 TTT	55 gIl :: 1049 TGT	39 rgL 1079	22 eThr   1098 CCTT	6 Leu     1148 CTT	Align seg 1	alignment_bl US-09-510-3	alignment_sc Percent Sim	ORIGIN		FEATURES source	, ,	TITLE JOURNAL COMMENT
eSerLysLeuValProTrpMetIleLeuGlySerLeuLeuTyrValSer 138 :        :::::::       :::::::	aLysValAlaSerValArgHisProLeuPheIleTrpLeuLysMetArgI 122 :    :::    :::    :::         :::         :::	AsnGluLeuGluLeuTrpLeuAlaThrTrpLeuGlyValPheTyrCysAl 105 :::	helleGluPhelleMetCysSerAlaAsnCysAlaIleLeuLeuPhelle 88   :::    :::::: TTTTTCTGTTTTTTTTTTTTTCCTGTTTTGT 968	<pre>gilePheLeuGlnLeuPheIlePheTyrValAsnValIleValIlePheP 72 :::   :::   rgrcTTTTGTGGTGTTTCTGGTTTGGTGTTCTTGTTGCTGTTTTT 1000</pre>	GLysMetAlaProLeuAspLeuLeuSerCysLeuAlaVal.SerAr 55	eThrAsnGlyIleIleValValValAsnGlyIleAspLeuIleLysHisA 39 	LeuIleIleTyrPheLeuLeuAlaValIleGlnPheLeuLeuGlyIlePh 22    :::::       :::::::::::::::::::::	1/1 to reverse of: BE734359 from: 1 to: 1544	_block: J-332-1 x BE734359/rev	scores: Quality: 141.50 Ratio: 0.963 Gaps: 18 Similarity: 48.515 Percent Identity: 26.403	222 g 59 t	/db_xref="taxon: 9606" /db_xref="taxon: 9606" /clone="IMAGE: 3840529" /clone="IMAGE: 3840529" /clone="Ilb="NIH_MGC_21" /tissue_type="choriocarcin /lab_host="DH10B (phage-re /note="Organ: placenta; ve Site_2: EcoR; cDNA made b Directionally cloned into following 5' adaptor: GGCA for average insert size 1. Ling Hong in the laborator of California, Berkeley) u (Stratagene) and Superscri	Location/Qualifiers 11544	Email: Robert_Strausberg@nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incytte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM530 row: 1 column: 02 High quality sequence stop: 54.	stitutes of (1999) bert Straus

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ISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 1502)
1 (bases 1 to 1502)
RS NIH-MGC http://www.ncbi.nlm.nlh.gov/MGC/.
RS NIH-MGC http://www.ncbi.nlm.nlh.gov/MGC/.
RAILonal Institutes of Health, Mammalian Gene Collection (MGC)
AL Unpublished (1999)
AL Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CLone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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alignment_block:
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High quality sequence stop: 59.
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Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies. "
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        found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov plate: LLCM52 row: m column: 20 High quality sequence stop: 148. Location/Qualifiers
                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Methazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 1652)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                              Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
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                                                                                             cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) CDNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
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                                                                                                     161 rGlnAsnAlaThrIleGlnLysGluAspThrLeuAlaIleGlnIlePheS 178
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900 | AF227119 Homo sapiens candidate

132953 | AC003015 Human BAC clone GSI

143719 | AC026787 Homo sapiens chromo

141747 | AC034214 Homo sapiens chromo
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! AF227140 Rattus norvegicus can
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AF227146 Rattus norvegicus cann
AF227132 Homo sapiens candidat
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        AF240765 Rattus norvegicus
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gb_pr1:AC004838
gb_htg16:AC073311
gb_pr4:AF227138
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KEYWORDS
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LOCUS AF227129
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alignment_block:
US-09-510-332-1 x AF227129
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                                                                                                                                                                                                                                            Quality: 1521.00
Ratio: 5.087
Percent Similarity: 100.000
                                                                      Homo sapiens candidate AF227129
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Submitted (21 JAN-2000) NIDCR,
Drive, Bethesda, MD 20892, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A novel family of mammalian taste receptors cell 100 (6), 693-702 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"G protein-coupled receptor; PCR-derived sequence; similar to an interval in BAC AC003015"

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SQNATIOREDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGSRVP
GRGAPISALLSILSFLIYFSHGMIKVFLSSLKFHIRRFIFLFFILVIGIYPSGHSLI
LIIGNPKLKQNAKKFLLHSKCCQ"
/1 000
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DEFINITION Human BAC clo
ACCESSION AC003015
                                                                                   seq_name:
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KEYWORDS
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                             132953 bp DN
clone GS1-113H23
                                 from
                                5p15
                            .2,
                                complete
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REFERENCE
AUTHORS
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                                                                                                                      Submitted (04-FEB-2000) Department of University, 4444 Forest Park Avenue, 9
                                                                                                                                                                                                                Direct Submission
Submitted (03-FEB-2000)
University, 4444 Forest
4 (bases 1 to 132953)
                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (20-OCT-1997) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
3 (bases 1 to 132953)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 132953)

Wamsley, P., Kramer, J., Elliott, G. and O'Brien, D.

The sequence of H. sapiens BAC clone GSI-113H23
                                                                                                                                                                                                  Waterston, R.
                                                                                                                                                                                                                                                                                              Waterston, R.
                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 132953)
Center project name: H_GS113H23
                                                Center: Washington University Genome : Center code: WUGSC Web site: http://genome.wustl.edu/gscContact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                 Department of Genetics, Park Avenue, St. Louis,
                                                                                                                                          f Genetics,
St. Louis,
                                                                                                     Sequencing Center
                                                                                                                                                                                                                                   Washington
Missouri 6
                                                                                                                                          63108,
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest. This sequence was finished as follows unless otherwise noted:

MAPPING INFORMATION:

information for this clone on, Department of Genetics, St. Louis MO. was provided by Dr. John D. Washington University School e E

Mapping information for this clone was also provided by Dr. Michael Lovett, Departments of Otorhinolaryngology, Molecular Biology and Oncology, University of Texas Southwestern Medical Center, Dallas

SOURCE INFORMATION:

(http://www.genomesystems.c Cell line: lymphoblastoid Haplotypes: two VECTOR: pBeloBAC This clone is from the first BAC library . com) from Genome Systems,

Selection:

chloramphenicol

VEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is GS1-330J10, 200 bp overlap. Actual start of this clone is at base position 1 of GS1-113H23; actual end is at 132953 of GS1-113H23.

This clone contains (NID:9454585). HSC022YA5 (NID:g1235481) and HS268ZDS

This clone contains polymorphisms with GS1-330J10
 Location/Qualifiers
 . 1. .132953

FEATURES source

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complement(5046.
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US-09-510-332-1 x AC003015
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Ratio: 5.087
Percent Similarity: 100.000
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                        LeuAlaValSerArgIlePheLeuGlnLeuPheIlePheTyrValAsnVa 67
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/rpt_family="L1"
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complement(63757.
/rpt_family="L1"
complement(63786.
/rpt_family="ALU"
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complement(52291.
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Gaps: 0
Percent Identity: 100.000
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KEYWORDS
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LOCUS AC026787 1.
  REFERENCE
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                                                                                                                                                 CCESSION
                                                               ORGANISM
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                                                                                                                                                                                                                                                                                                           yIleTyrProSerGlyHisSerLeuIleLeuIleLeuGlyAsnProLysL 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATATACCCTTCTGGACACTCTCTCATCTTAATTTTAGGAAATCCTAAAT 55700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCTGGCAGGGGTGCACCCATCAGCGCGTTGCTGTCTATCCTGTCCTTCC 55550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lProGlyArgGlyAlaProIleSerAlaLeuLeuSerIleLeuSerPheL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuGlyArgHisThrArgGlnMetArgAsnThrValAlaGlySerArgVa 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MetValProTyrPheLeuArgLysPhePheSerGlnAsnAlaThrIleG1 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ValPheTyrCysAlaLysValAlaSerValArgHisProLeuPheIleTr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGGTCCCATACTTCCTAAGGAAATTTTTCTCCCAAAATGCCACAATTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLeuLySMetArgIleSerLySLeuValProTrpMetIleLeuGlySerL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATTGTTATCTTCATAGAATTCATCATGTGTTCTGCGAATTGTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTGAAGATGAGGATATCCAAGCTGGTCCCATGGATGATCCTGGGGTCTC
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                                                                                                                                                              Homo sapiens chromosome 5 cl
SEQUENCE, 10 ordered pieces.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 143719)
                                                             Homo sapiens
                                                                                                AC026787.3 GI:9256685
HTG; HTGS_PHASE2; HTGS_DRAFT
                                                                                                                                                                                                          143719 bp
                                                                                                                                                                                    DNA HTG
5 clone CTD-2143L24,
                                                                                                                                                                                    18-JUL-2000
WORKING DRAFT
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          alignment_block:
US-09-510-332-1 x AC026787
                                                                                                                                                                                                   BASE COUNT
ORIGIN
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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
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                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                        FEATURES
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                                                                                                                                                                                                                                                                                                                                                  source
                                                                      Similarity:
                                                                                                                                                                                                                                                                                                                                                                             * provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

1 1768 contig of 1768 bp in length

1 1869 18093 contig of 16225 bp in length

* 18194 54185 contig of 35992 bp in length

* 54186 54285 gap of unknown length

* 54186 54285: gap of unknown length

* 84033 84132 gap of unknown length

* 84033 84142 contig of 29747 bp in length

* 84033 89414 contig of 5282 bp in length

* 89415 97457 contig of 7943 bp in length

* 89515 97457: contig of 7943 bp in length

* 132197 134948: contig of 34539 bp in length

* 132197 134948: contig of 2752 bp in length

* 132197 134948: contig of 2752 bp in length

* 132197 134948: contig of 2752 bp in length

* 13247 139346: gap of unknown length
                                                                      Quality: 1516.00
Ratio: 5.070
nilarity: 100.000
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Consensus quality: 142137 bases at least Q30
Consensus quality: 142139 bases at least Q20
Estimated insert size: 145000; pulse field gel estimation
Estimated insert size: 143119; sum-of-contigs estimation
Quality coverage: 5.41 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 10 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (24-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 18, 2000 this sequence version replaced gi:7711997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Project Information Center Project Name: 682749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Joint Genome Institute Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 143719)
DOE Joint Genome Institute.
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Sequencing of Human Chromos
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                         44478
                                                                                                                                                                                                                         Ø
                                                                                                                                                                                                                /clone="CTD-2143L24"
/clone_lib="CalTech human
28860 c 28265 g 41210
                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                               Length: 299
Gaps: 0
Percent Identity: 99.666
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906 others
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Align seg 1/1

to: AC026787

from: 1

; 0:

143719

4517

ATGCTAGAGTCTCACCTCATTATCTATTTTCTTCTTGCAGTGATACAATT 

4566

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4667

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leLeuLeuPheIleAsnGluLeuGluLeuTrpLeuAlaThrTrpLeuGly 100

4617

TCTTCTTGGGATTTTCACAAATGGCATCATTGTGGTGGTGAATGGCATTG eLeuLeuGlyIlePheThrAsnGlyIleIleValValAsnGlyIleA 34

4616

4716 67 4666

| IlleValIlePhePheIleGluPheIleMetCysSerAlaAsnCysAlaI 84

GATTGTTATCTTCATAGAATTCATCATGTGTTCTGCGAATTGTGCAA 4766

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REFERENCE
AUTHORS
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                      Consensus quality: 129482 bases at least Q40
Consensus quality: 137633 bases at least Q30
Consensus quality: 139230 bases at least Q30
Consensus quality: 139230 bases at least Q20
Estimated insert size: 128750; agarose-fp estimation
Estimated insert size: 141047; sum-of-contigs estimation
Quality coverage: 5.08 in Q20 bases; agarose-fp estimation
Quality coverage: 4.64 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor:
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1 1582: contig of 21582 bp in length
* 21583 21682: gap of unknown length
* 34006 34105: contig of 12323 bp in length
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SEQUENCE, 16 ordered pieces.
AC034214
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Mammalla; Eutheria; Primates; Q
1 (bases 1 to 141747)
DOE Joint Genome Institute.
Sequencing of Human Chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (05-APR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA on Jul 18, 2000 this sequence version replaced 91:7712070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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DOE Joint Genome Institute.
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2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center Project Name: 628051
Center clone name: CITB-H1_2001E22
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34006
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92578:
92678:
92678:
103695:
103795:
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                                                                                                                                                                                                                                                                                                                      34105: gap of unknown length
37105: contig of 3000 bp in
37205: gap of unknown length
39674: contig of 2469 bp in
                                                                                                                                                            58513:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                 7: gap of unknown length
3: contig of 1316 bp in length
3: gap of unknown length
5: contig of 15272 bp in length
6: gap of unknown length
8: contig of 18593 bp in length
8: gap of unknown length
8: gap of unknown length
5: contig of 11017 bp in length
5: gap of unknown length
                                                                                                                                                                                              gap of unknown contig of 6754 gap of unknown contig of 6009 gap of unknown contig of 4360
gap of contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NA HTG 18-JUL-2 Clone CTD-2001E22, WORKING DRAFT
                                                                                                                                                                                                f unknown
g of 6009
f unknown
g of 4360
unknown
of 2437
                                                                                                                                                                                                    bp in length
                                                                                                                                                                                                                                           length
bp in length
                                                                                                                                                                                                                                                                                    bp in
                                                                                                                                                                                                                                                                                                                          bp in length
đđ
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  length
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alignment_block:
US-09-510-332-1 x AC034214
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
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Percent Similarity:
                                                          39607
                                                                                                                 39557
                                                                                                                                                                      39508
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                                                                                                                                            134
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                                                                                                                                                                                                                       GlnLysGluAspThrLeuAlaIleGlnIlePheSerPheValAlaGluPh
                                                     TTATGGTCCCATACTTCCTAAGGAAATTTTTCTCCCAAAATGCCACAATT
                                                                                                                          euLeuTyrValSerMetIleCysValPheHisSerLys.TyrAla.Glyp 150
                                                                                                                                                                                                                                                                            lIleValIlePhePheIleGluPheIleMetCysSerAlaAsnCysAlaI 84
                                                                   heMetValProTyrPheLeuArgLysPhePheSerGlnAsnAlaThrIle 166
                                                                                                             TGCTATATGTATCTATGATTTGTGTTTTCCATAGCAAACTATGCAGGGAT
                                                                                                                                                                  GTTGAAGATGAGGATATCCAAGCTGGTCCCATGGATGATCCT.GGGTCTC
                                                                                                                                                                                  PLeuLysMetArgIleSerLysLeuValProTrpMetIleLeuGlySerL 134
                                                                                                                                                                                                                                                                                                                                  GATTGTTATCTTCATAGAATTCATCATGTGTTCTGCGAATTGTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTTGATCAAGCACAGAAAAATGGCTCCGCTGGATCTCCTTCTTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              eLeuLeuGlyIlePheThrAsnGlyIleIleValValValAsnGlyIleA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MetLeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIleGlnPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGCTAGAGTCTCACCTCATTATCTATTTTCTTCTTGCAGTGATACAATT
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Ratio: 4.417
nilarity: 87.748
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106333
121674
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124115
124215
131888
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/organism="Homo sapiens"
/ob_xref="taxon:9806"
/chromosome="5"
/clone="CTD-2001E22"
/clone="CTD-2001E22"
a 28372 c 28509 g 41923 t
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121673: contig of 15341 bp in length
121773: gap of unknown length
124114: contig of 2341 bp in length
124214: gap of unknown length
131887: contig of 7673 bp in length
131987: gap of unknown length
141747: contig of 9760 bp in length.
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Gaps: 4
Percent Identity: 84.768
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DEFINITION
ACCESSION
VERSION
KEYWORDS
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REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
 BASE COUNT
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LOCUS AF227149
                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_ro:AF227149
                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 eSerValProLeuLeuIlePheLeuPheAlaValLeuLeuIlepheS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTAAAGTTTCACATCAGAAGGTTCATCTTTCTGTTCTTCATCCTTGTGAT
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                      Submitted (21-JAN-2000) NIDCR, Drive, Bethesda, MD 20892, USA
                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                   Adder, E., Hoon, M.A., Mueller, K.L., and Zuker, C.S.
                                                                                                                                                                                                                                                                                                                                                                                         A novel family of mammalian taste receptors Cell 100 (6), 693-702 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                              Zuker,C.S
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Adler, E., Hoon, M.A.,
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                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 1008)
 224
                                                      /translation="MMEGHMLFFLLVVVVQFLTGVLANGLIVVVNAIDLIMWKKMAPL
DLLFCLATSRIIGUETEAQUGLSCLVRHTLFADNVTFVYIINELSLMFATWLGVF
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SKNTTRVRPAHATLLSVFVFGLTLPFLIFTVAVLLLSSLMNHSRQMRTMVGTREPSR
                           LGNPKLKRNAKTFIVHCKCCHCARAWVTSRNPRLSDLPVPATHHSANKTSCSEACIMP
                                         HALVSAMLSILSFLILYLSHDMVAVLICTQGLHFGSRTFAFCLLVIGMYPSLHSIVLI
                                                                                                                    /product="candidate taste receptor T2R19"
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/db_xref="GI:7262645"
                                                                                                                                                                                                                              /organism≔"Mus musculus'
/strain="129/SvJ"
                                                                                                                                                                 /codon_start=]
                                                                                                                                                                              /note="G protein-coupled receptor"
                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                            db_xref-"taxon:10090
 252
 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
Rodentia;
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209
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taste
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receptor T2R19
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                                                                                                                                                                                                                                                                                                    10 Center
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alignment_block:
US-09-510-332-1 x AF227149
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                                                                                                                                                                                                                                                                                                                                                                                                  451
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|||||||||||||||:::||||||||||:::|||||
| GCTGAAGATGAGGATATCCAGGTTGGTGCCATGGCTGATCCTGGCATCTG 400
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                                                                                                                                                 gValProGlyArgGlyAlaProIleSerAlaLeuLeuSerIleLeuSerP
                                                                                                                                                                                                          SerLeuGlyArgHisThrArgGlnMetArgAsnThrValAlaGlySerAr
                                                                                                                                                                                                                                                                             heSerValProLeuLeuIlePheLeuPheAlaValLeuLeuLeuIlePhe 199
                                                                                                                                                                                                                                                                                                                                                                                                  CTTCCTAAGCAAATCTTTATAAGCTTTTTTTCTAAAAATACAACTCGGGT 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGTCTATGTAACTGTTACTACTTTCATCCATAGCAGAGAGACTTCAGAA 450
LeuLysPheHisIleArgArgPheIlePheLeuPhePheIleLeuValII
                                                   TCCTCATCCTCTCTCTCCCATGACATGGTAGCTGTTCTGATCTGTACC
                                                                                 heLeuIleLeuTyrPheSerHisCysMetIleLysValPheLeuSerSer
                                                                                                                      GGAACCTAGCAGACATGCCCTCGTCAGTGCGATGCTCTCCATTCTGTCAT
                                                                                                                                                                                         TCCCTGTGGAACCACAGCCGGCAGATGAGG...ACTATGGTGGGAACTAG
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3.218
81.271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adler, E., Hoon, M.A., Mueller, K.L., and Zuker, C.S.
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Mammalia; Eutheria;
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Rattus norvegicus
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Sciurognathi; Muridae;
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Homo sapiens chromosome 7 clone RP11-472F21,
SEQUENCE, 18 unordered pieces.
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Direct Submission
Submitted (12-NOV-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
On Jul 15, 2000 this sequence version replaced gi:8954416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Washington University Genome Sequencing Center Center code: WUGSC
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Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site:http://genome.wustl.edu/gsc/index.shtml
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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FEATURES
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117069 AAATGGATTTCTTATCATTGTTAACTGTAATGAATTGATCAAACATAGAA 117020
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                                                         rAsnGlyIleIleValValValAsnGlyIleAspLeuIleLysHisArgL 40
                                                                                                                                     ATTCTTCATATTATCATGATGTCAGCAGAATTCTTCACAGGGATCACAGT 117070
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/db_xref="taxon:9606"
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[7242. .24045
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68.771
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151171. .180438
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133602. .151070
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.e="assembly_name:Contig14"
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                                                                                                                                    116240 G 116240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  euPheIleAsnGluLeuGluLeuTrpLeuAlaThrTrpLeuGlyValPhe 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PheLeuGlnLeuPheIlePheTyrValAsnValIleValIlePhePhe.. 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  erArgValProGlyArgGlyAlaProIleSerAlaLeuLeuSerIleLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCATTAATATTTCCTCTAGCCATATTTGTGATGTGCACTTCTATGTTACT 116535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTCTGTGAGCATTGCATCTGTGTGTCGAGGTAGATTACGCTAAAAATGT 116670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..TyrValSerMetIleCysValPheHisSerLys.TyrAlaGlyPheMe 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ysGluAspThrLeuAlaIleGlnIlePheSerPheVal......Ala 181
                                                                                                                                                                                                                                                                                                                                                                                           GlyAsnProLysLeuLysGlnAsnAlaLysLysPheLeuLeuHisSerLy 296
                                                                                                                                                                                                                                                                                                           AGGACATAATGGCAGCATATCCCTCTGGCCACTCGGTTATAATAATCTTG
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AC005541 110626 bp DNA PRI Homo sapiens clone RG044L22, complete sequence.
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DEFINITION

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US-09-510-332-1 x AC005541/rev
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ORIGIN
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                                                                                                                                                                                                   4192 ACTCCTTTACGTCAAAATAATTTATGGTGCAGCAATGATGTTCCTTTGGA 4143
                                                                                                                                                                                                                                                                         4242 GGTCTGCAGATGGTGTTAATGGTACAAAGTTTTTTCTCTGTGTTCTTTCC 4193
                                                                                                                                                                                                                                                                                                                                                                                                                           4342 AAATGGATTTCTTATCATTGTTAACTGTAATGAATTGATCAAACATAGAA 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4392 ATTCTTCATATTATCATGATGTCAGCAGAATTCTTCACAGGGATCACAGT 4343
                                                                                                                                                                                                                                                                                                                                                 86
                                                                                                                                                                                                                                                                                                                        57
                                                                                                                                                                                                                                                                                                                                                                                                                                              23 rAsnGlyIleIleValValValAsnGlyIleAspLeuIleLysHisArgL 40 :||||||::::::::::::|||||||
TACTGCCTCAAGATTTCAGGCTTCACTCAGTCCTGTTTTCTTTGGTTGAA
                                                                                       TyrCysAlaLysValAlaSerValArgHisProLeuPheIleTrpLeuLy 119
                                                                                                                            TGTTTTTAGCTCTATCAGCCTATGGTTTGCCACTTGCCTTTCTGTATTT
                                                                                                                                                             euPheIleAsnGluLeuGluLeuTrpLeuAlaThrTrpLeuGlyValPhe 102
                                                                                                                                                                                                                                                                                                            PheLeuGlnLeuPheIlePheTyrValAsnValIleValIlePhePhe. 72
                                                                                                                                                                                                                                      .....IleGluPheIleMetCysSerAlaAsnCysAlaIleLeuL 86
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Waterston,R.H.
Direct Submission
Submitted (14-JAN-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Jan 14, 1999 this sequence version replaced gi:3907453.
Location/Califiers
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Eukaryota; Methazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 110626)
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Direct Submission
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AC005541.1 GI:4156136
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Homo sapiens
                                                                                                                                                                           Zuker,C.S.
A novel family of mammalian taste receptors
Cell 100 (6), 693-702 (2000)
                                 Direct Submission
Submitted (21-JAN-2000) NIDCR,
Drive, Bethesda, MD 20892, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1. (bases 1 to 951)
                                                                                                                     Adler, E., Hoon, M.A., Mueller, K.L., Chandrashekar, J., and Zuker, C.S.
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∕organism="Homo sapiens"
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primer_bind
BASE COUNT
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TSSRDPTTEAHKRAIRIILSFEFELFLLYFLAFLIASFGNFLPKTKMAKMIGEVMTMFY
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similar to an interval in PAC AC004979"
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CTTCAGAAAGAAGAGAGTGATTATCTGATCCATGTTCTTGGGACTC
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                                                                               Waterston,R.
Direct Submission
Submitted (13-JAN-1999) Department of Genetics,
University, 4444 Forest Park Avenue, St. Louis,
4 (bases 1 to 82419)
             Direct Submission
Submitted (21-DEC-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6
On Jan 13, 1999 this sequence version replaced g1:3264780.
                                                                                                                                                                                                     Direct Submission
Submitted (12-JUN-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 82419)
Du,H., Duckels,G. and Kock,J.
The sequence of Homo sapiens PAC clone RP5-1154E9
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Mammalia; Eutheria; Primates;
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Catarrhini; Hominidae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The clone sequenced to the left is RP5-894A10, 200 bp overlap; the clone sequenced to the right is unknown. Actual start of this clone is at base position 103168 of RP5-894A10; actual end is at 82419 of RP5-1154E9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   one male donor.

The clone may be obtained either from Genome Systems, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone was derived from human PAC library RPCI-5, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from the company of the second se
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NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://www.genomesystems.com) or Research Genetics, Inc. (http://www.resgen.com); or from Pieter de Jong.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE INFORMATION:
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Contact: saplens@watson.wustl.edu
----- Summary Statistics
Center project name: H_DJ1154E09
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3226. .3272
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801. .1104
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/clone="RP5-1154E9"
/clone_11b="RPCI-5"
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1. .82419
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/db_xref="taxon:9606"
/chromosome="7"
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23385. .29503
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/note="match to EST AA649071 (NID:g2575500) ns42h02.s1"
3498. .3878
rpt_family="L1"
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3587. .3874
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3365. .3878
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/note="match to EST AI031578 (NID:g3249790) ow06e12.xl"
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155 eLeuArgLysPhePheSerGlnAsnAlaThrIleGlnLysGluAspThrL 172
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                                                                                                                                                    MetIleCysValPheHisSerLysTyrAlaGlyPheMetValProTyrPh 155
                                                                                    CTCTATTCTGTCTTTAGGGGAATTGAGGCCACCAGGAATGTGACTGAACA 18084
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36544. .36581
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34523. .34757
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38203. .38257
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Homo sapiens candidate taste receptor T2R8 gene,
AF227134
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                                                                                                                                                                                                                                                                                                                                                                             A novel family of mammalian taste receptors Cell 100 (6), 693-702 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="G protein-coupled receptor; PCR-derived similar to an interval in BAC AC006518" (codon_start=1 /product="candidate taste receptor T2R8" /protein_id="AAF43907.1" /db_xref="GI:7262615"
                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12"
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primer_bind
BASE COUNT
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US-09-510-332-1 x AF227134
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Submitted (21-JAN-2000) NIDCR,
Drive, Bethesda, MD 20892, USA
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Adler, E., Hoon, M.A.,
and Zuker, C.S.
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Adler E., Hoon, M.A., Mueller, K.L., Chandrashekar, J., Zuker, C.S.
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/translation="madkvqttllflavgefsygilgnafiglvncmdwvkkrkiasi
Dilifsklaiskiclicvilldocfilvlypdvvatgkemriidfemtlinhlstwfatc
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KAKRKTNLTWSCRVNKTQHASTKLFLNUATLLPFCVCLMSFFLLILSLERHIRRNQLS
ATGCRDPSTEAHVRALKAVISFLLLFIAYYLSFLIATSSYFMPETELAVIFGESIALI
                                                                                                                                      1. .957
/note="G protein-coupled receptor; PCR-derived similar to an interval in BAC AC006518"
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/db_xref="GI:7262613"
                                                                                                                                                                                                                       /map="12p13"
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                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 LeuAlaValIleGlnPheLeuLeuGlyIlePheThrAsnGlyIleIleVa
   669
                                   216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       euGluLeuTrpLeuAlaThrTrpLeuGlyValPheTyrCysAlaLysVal 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IlePheTyrValAsnValIleValIlePhePheIleGluPheIleMetCy 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         spLeuLeuLeuSerCysLeuAlaValSerArgIlePheLeuGlnLeuPhe 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lvalValAsnGlyIleAspLeuIleLysHisArgLysMetAlaProLeuA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                            sLeuValProTrpMetIleLeuGlySerLeuLeuTyrValSerMetIleC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTAATTTCTTTCACCCACTTTTCCTCTGGATGAAGTGGAGAATTGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaSerValArgHisProLeuPheIleTrpLeuLysMetArgIleSerLy 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAAGTATCTGGTTTGCAACCTGCCTCAGCATTTACTATTTCTTCAAGATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATACTATTAGATTGTTTTATATTGGTGCTATATCCAGATGTCTATGCCAC
                                                                                                                                                                        heSerValProLeuLeuIlePheLeuPheAlaValLeuLeuLeuIlePhe 199
                                                                                                                                                                                                                                              eGlnLysGluAspThrLeuAlaIleGlnIlePheSerPheValAlaGluP 183
                                                                                                                                                                                                                                                                                                                 PheMetValProTyrPheLeuArgLysPhePheSerGlnAsnAlaThrIl 166
                                                                                                                                                                                                                                                                                                                                                        CTGTGTTTATTAGCCTTCCAGCCACTGAGAATTTGAACGCTGATTTCAGG 471
                                                                                                                                                                                                                                                                                                                                                                                                                            GGTGATTTCCTGGATTCTACTGGGGTGCGTG......GTTCTCT 421
                                                                                                                                                                                                                AAATAAAACTCAACATGCTTCTACCAAGTTATTTCTCAACCTGGCAACGC
                                                                                                                                                                                                                                                                                   TTTTGTGTGAAGGCAAAGAGGAAAACAAACTTAACTTGGAGTTGCAGAGT 521
                                                                                                     SerLeuGlyArgHisThrArgGlnMetArgAsnThrValAlaGlySerAr
AGACCCCAGCACAGAAGCCCCATGTGAGAGCCCCTGAAAGCTGTCATTTCCT
                               gValProGlyArgGlyAlaProIleSerAlaLeuLeuSerIleLeuSerP 233
                                                                                                                                          TG...CTCCCCTTTTGTGTGTGCCTAATGTCCTTTTTCCTCTTGATCCTC
                                                                         TCCCTGCGGAGACATATCAGGCGAATGCAGCTCAGTGCCACAGGGTGCAG
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Percent Identity: 32.653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                roLysLeuLysGlnAsnAlaLysLysPheLeu 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens chromosome 20 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (23-NOV-1999) Human Genome Sequencing Center, Department Submitted (14-NOV-1999) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Baylor Plaza, Houston, TX 77030, USA
On Aug 26, 2000 this sequence version replaced gi:9719589.
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Bodota,B., Bouck,J., Bowle,S., Brooks,A., Buhay,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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Sequencing vector: M13; L08821
Chemistry: Dye-primer Bodipy: 12% of reads
Chemistry: Dye-terminator Big Dye: 86% of reads
Chemistry: Dyerterminator Big Dye: 86% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 129880 bases at least Q40
                                                                                                                                                                                                                                                                    web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ project Information
Center project name: HMOY
Center clone name: RP13-81N3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Baylor College of Medicine Center code: BCM
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    Genome Center

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Bowie,S., Brooks,A., Buhay,C., Bunac,C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chacko, J., Chen, Z., Cox, C.,
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WORKING DRAFT SEQUENCE,
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alignment_block:
US-09-510-332-1 x AC016145/rev
                                                                                               alignment_scores:
                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                      FEATURES
                                                  Percent Similarity:
                                                                                                                                                                                                                                       source
                                                                  Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length (see http://www.lbgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a "vorking draft" sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Consensus quality: 145651 bases at least Q30 Consensus quality: 151922 bases at least Q20 Estimated insert size: 154982; sum-of-contigs estimation Estimated insert size: 155000; agarose-fp estimation Quality coverage: 3.9x in Q20 bases; agarose-fp estimation Quality coverage: 3.4x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                        /clone="RP13-81N3"
30129 c 29217 g
                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12"
                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                  Percent Identity: 32.653
                                                                                                                                                                                                                                                            : gap of unknown : contig of 1759
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g unknown length
g of 4402 bp in la
f unknown length
g of 3400 bp in la
f unknown length
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f unknown length
g of 10973 bp in
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f unknown length
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                                                                                                                                                           AGCTACTTTATGCCAGAGACGGAATTAGCTGTGATTTTTGGTGAGTCCAT
                                                                                       eGly...IleTyrProSerGlyHisSerLeuIleLeuIleLeuGlyAsnP
                                                                   AGCTCTAATCTACCCCTCAAGTCATTCATTTATCCTAATACTGGGGAACA 57633
                                                                                                                                                                                                        LeuLysPheHisIleArgArgPheIlePheLeuPhePheIleLeuValIl 266
                                                                                                                                                                                                                                                     TCCTTCTCCTCTTTATTGCCTACTATTTGTCCTTTCTCATTGCCACCTCC
                                                                                                                                                                                                                                                                                                    heLeuIleLeuTyrPheSerHisCysMetIleLysValPheLeuSerSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TG...CTCCCCTTTTGTGTGTGCCTAATGTCCTTTTTTCCTCTTGATCCTC 57883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTTGTGTGAAGGCAAAGAGGAAAACAAACTTAACTTGGAGTTGCAGAGT 57980
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AC006518 173735 bp DNA PRI 01-MAY-1999
Homo sapiens 12p13 BAC RPCI11-144023 (Roswell Park Cancer Institute
Human BAC Library) complete sequence.
AC006518
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SOURCE ORGANISM ACCESSION VERSION KEYWORDS Homo sapiens AC006518.17 GI:4713939

DEFINITION

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 173735)

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE AUTHORS Muzny,D., Arenson,A.D., Bouck,J., Bunac,C., Chen,Z., Ding,Y., Dugan,S., Durbin,J., Forcum,J., Garcia,C., Gorrell,J.H., Correll,J.L., Hernandez,J., Issar,A., Jackson,L., Kneitz,S., Kondejewski,N., Lau,S., Leal,B., Lee,E., Lichtarge,O., Liu,W., Logan,O., Lu,J., Marondel,I., Martinez,C., Merscher,S., Miller,A., Montgomery,K., Oswal,G., Pampell,L.R., Parish,B.J., Perez,L., Mashid,N.D., Rives,C., Scherer,S.E., Shen,H., Shim,C., Simon,M., Vo,Q., Williamson,A., Worley,K.C., Xhang,A.M., Yang,R., Yu,W., Zhou,X., Kucherlapati,R., Nelson,D. and Gibbs,R.A.

REFERENCE JOURNAL 2 (bases 1 to 173735)

Worley,K.C.

Direct Submitssion
Submitted (05-FEB-1999) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 173735)
Worley,K.C.

TITLE JOURNAL AUTHORS Direct Submission

REFERENCE AUTHORS TITLE

Submitted (01-MAY-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 173735)
Worley,K.C.
Direct Submission
Submitted (01-MAY-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Apr 29, 1999 this sequence version replaced gi:4589934.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email

Phrap Value Range

COMMENT

gc-help@bcm.tmc.edu

JOURNAL

CHONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:
STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green

unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the

annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.

QUALSTAT-REPORT------

	ប់	:	Position 31176 31177 104155	Contig length: Phrap values i Average error Fraction of Ph Number of cons Number of N's
5 10	10001 9001 8001 7001 5001 5001 5001 2001 1001 1 * * * *	- Distribution of Quality $<$ 40	Original+Context Original+Context gtgggttggg(n)agaggggag tgggttgggn(a)gagggggagg tgggtttcact(n)tgttgtcctc	Contig length: Phrap values in estimate: Average error rate (BCM Phrap estim Fraction of Phrap values less than Number of consensus changing edits: Number of N's in consensus:
15 20	* * *	Quality < 4	changing entext agagggggag agaggggagg	atistics ap estimate): ss than 40: sg edits:
25 30	****	0 Bases -	edits Edite g gtgggg g tgggg c gagtt	e)
35 40			Edited+Context gtggggtggg(g))ggaggggag tggggtgggg(g))gaggggagg	173735 167393 0.000263256 0.0395058

repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region			source	FEATURES	Version:
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Ratio:
Percent Similarity:
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US-09-510-332-1 x AC006518/rev
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complement(30369. .30398)
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complement(28088. 28123)

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complement(28124. 28214)

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2.000
58.750
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14232 .14649
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18679 ..18844
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3. .28087
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Gaps: 10
Percent Identity: 31.562
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289	273 HisSerLeuIleLeuIleLeuGlyAsnProLysLeuLysGlnAsnAlaLy
5052	1 AGTTA
. 260 1 5102	SPheHisIleArgArgPheIlePheLe :::     ::   TTGATGACCTTTAGCTATCT
e 248     5143	'sValPheLeuS 
u 231 T 5178	215 erArgValProGlyArgGlyAlaProIleSerAlaLeuLeuSerIleLeu 
S 215	198 ePheSerLeuGlyArgHisThrArgGlnMetArgAsnThrValAlaGly: :
1 198 : T 5278	PAG  EuI
a 181 . 5319	alleGlnIlePheSerPheValAl :::::::   ::::: CTTTAACCTGTTTGCAATT
T 165	sPhePheSerGlnAsnAla
1 148 A 5374	
. 142 T 5424	1 ; AATAGTA
134 CA 5474	119 sMetArgIleSerLysLeuValProTrpMetIleLeuGlySerLeu
y 119	103 TyrCysAlaLysValAlaSerValArgHisProLeuPheIleTrpLeuLy 
ne 102       C 5574	87PheIleAsnGluLeuGluLeuTrpLeuAlaThrTrpLeuGlyValPhe 
86 3A 5624	74 uPheIleMetCysSerAlaAsnCysAlaIleLeuLeu
G1 74 CC 5674	58 LeuGlnLeuPheIlePheTyrValAsnValIleValIlePhePheIleG
he 57 GT 5721	41 etAlaProLeuAspLeuLeuSerCysLeuAlaValSerArgIleP
'SM 41  :  GA 5771	24 nGlyIleIleValValValAsnGlyIleAspLeuIleLysHisArgLy:

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JOURNAL
MEDLINE
REFERENCE
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ACCESSION
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BASE COUNT 2
ORIGIN
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS AF227135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_pr4:AF227135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
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                                                                                                                                                                                              alignment_block:
US-09-510-332-1 x AF227135
                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
                                                                                                                                                         Align seg 1/1 to: AF227135
                                                                                                                                                                                                                                                        Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ::::::||
5001 CAGAATGCTG 4992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 sLysPheLeu 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             primer_bind CDS
22
                                                                                                  8 IleTyrPheLeuLeuAlaValIleGlnPheLeuLeuGlyIlePheThrAs
                                                                             AF2Z7135 939 bp DNA PRI 18-MAR-2000
Homo: sapiens candidate taste receptor T2R9 gene, complete cds.
AF2Z7135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 939)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF227135.1 GI:7262616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (21-JAN-2000) NIDCR, prive, Bethesda, MD 20892, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adler, E., Hoon, M.A., Mueller, K.L., Chandrashekar, J., Ryba, N.J.P. and Zuker, C.S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A novel family of mammalian taste receptors Cell_100 (6), 693-702 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adler, E., Hoon, M.A., Mueller, K.L., Chandrashekar, J., Ryba, N.J. and Zuker, C.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                             Quality:
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                                                                                                                                                                                                                                                                                                                                                                                               248
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1.905
62.102
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                                                                                                                                                              from: 1
                                                                                                                                                                                                                                                        Length: 314
Gaps: 9
Percent Identity: 32.166
                                                                                                                                                              to: 939
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	267	765	37	20 r	03 g	87 L 71 T	70 s 42 T	63 n 92 C	54 ·	37 a : 19 T	20 t 72 A	04 CY:	37 he 	'0 eP 22 TA	8 Le	1 etA ::: 2 TTT
TCATI	Ξ.	uLysP : TCTGA	CTCAT	gGly AGAG	HisT       CACA	euLe :::: TTAT	PThr         AACC	AlaT	AAGAAT	lSerM :   : CTCTT	Argīl :::   AAGAT	SAla	Ile	hep : CAT	uGln         	lap :: CCT
PTYPP  -::   TTCC	3	heHi :: TTCC	CGTG	Alap     GCCC	hrAr   ::  CCAA	uIle :::: CCTT	LeuAl	hrIle	TGATG	MetIl :::   TTAAT	LeSer   :::  CAAC	Lysv    :  AAGA	SnGl   ::  ATAA	heIle ;; ATGGC	Leup	roLeu ::: TGATT
CATO	ose	SIle	TyrP  - -: TACT	roll:	gGln) :    :GCAG	PheLe    TGCCT	aIl ::	eGln. ::: :AAAT	ATAT	eCys	LysL    :  AAGG	a1A1 ::   TAGC	uLeu ; TTC!	GluPhe ::: AATAGC	heIl     TAAT	Asp     GAC
ñ٠	GLy	ArgAr :: :GGAAA	heSer :: ACCCA	eSerA :   GAGGG	MetAr :::   ;ATTCG	euPhe   :::  GATC	.eGlnI : ::	7 :	····	Vale	euVa :::: TCAT	aSer  :::  CAAT	GTC	GT::I	e    ATCAT	LeuLe :::: ATCA
ATT	Hiss	rgPhe ::::: AATTA	rHisc A	1 = S	gAs    ACI	Ala :::	lePhe ::::: TGATG	AAAGTG	TyrP     TATC	heHi.	lProT : GCTTG	ValAr ::: ATATC	euTrp        TCTGG	eMetc :::: GCTAG	TAG	euLeu ::    TCCTG
ATT	erLeu   :::	IleP :::::	ysMe	uLeu ; AAAG	hrv ATG	alLe :: TTTT	Ser	AGTA	heLe	sSerl	LProTrpMet:	rgHis      CGCAC	oLeuA  :::: GTTTA	yss   TAP	····	Ser
ATTC	IleI	heLe :::: TGAT	G:: £1	SerI :::: GCAG	alAl :::: CTAC	uLeu :	PheV	AAAATT	LeuArgI	LysTy	CTT	ProL	laThr ::::: CTTCT	erAla     GCATT	PheT    : TTCT	CysLe
AAT	   euI1	uPhe :::: GATT	eLysV	leLe: :::: TGAT	aGlys :    AGGGT	LeuIl    :: TTACT	'alAla	 PCCAG	LysPh      AAAGT	rAla	LeuG      CTGG	euPh ::   TTTT	Trp	AlaAsnCys <i>i</i> CATTGTGAAT(	yrva :::: TTAT	uAla\       GGCC/
AIG	eLeu	PheI GGTG	alPhe   ::: TTATG	uSerP :   CATCT	SerAr    TTCAG	LePhe ::    !TTTC	aGluPhe	GTAC	heP	GlyPh :: AT	lyse       GGTC	eIle  ::: CTTC	LeuG    : CTCA	ysala ::: ATGTT	lAsnV : : GCTGC	Valse :::   ATCTC
Š	GlyAs	leLeu ::: :ACATA	eLeuS :   GACCT	PheLe	gval      AGAC	SerI	· Se	TTTC	Phes CATG	eMe : TAG	rLeu!  ::: CTTT	TrpLe	LyVal	Ile	/alil :::::: CTCTT	erArg        CAGA
TAG	nPr	GT Va	SerSe	uIle  :::	ProG	euG  - TAG	rval	LysG    :	erGl :::: AAGA	tVall	LeuT	euLys       TGAAG	1PheT:	LeuLe	eVa ; TCC	ilep
CAAG	-£	lileG      AACTG	SCGC	CIC	HYA :: GTA	lyAr    TTAG	Pro	luA :: AGT	nAs :	Pro	угV :	ÇI	AT Y	AT UP	11	he 5
	283 864	267 814	250 764	236 720	220 670	203 620	186 570	170 541	163 491	153 441	137 418	120 371	103 321	87 271	70 221	71

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OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
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                                                                                                                                                                                                                                                         Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
376
371.5
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6::
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     March 15, 2001, 12:57:24; Search time 71 Seconds (without alignments) 493.594 Million cell updates/sec
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Match Length DB
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Gapop 10.0 , Gapext 0.5
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1 MLESHLITYFLLAVIQFLLG......GNPKLKQNAKKFLLHSKCCQ 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_archea:*
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sp_unclassified:*
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                                                                                                                                                                                                                                                                                                                                                                                                                sp_plant:*
sp_rodent:*
  335
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Q9NYW1
1 Q9JKW1
1 Q9JKE9
Q9NYV9
1 Q9JKT7
1 Q9JKT9
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                                        Q9jkul rattus norv
Q9nyw6 homo sapien
Q9nyw3 homo sapien
Q9nyw3 homo sapien
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Q9jkt6 rattus norv
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Q9jkt8 rattus norv
Q9jkt9 rattus norv
Q9jkt9 rattus norv
                                                                                                                                                                                                                         Q9nyw7 homo sapien
Q9jkt2 mus musculu
                                                                                                                                                                                                                                                               Description
    Q9jkf0 rattus norv
Q9nyv7 homo sapien
Q9nyv8 homo sapien
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	120 5	120.5	121.5	121.5	122	122.5	122.5	124	124	125	125	125	128.5	130.5	134	182	217.5	230.5	231.5	237.5	242.5	264.5	266.5	289	294	298
;	7.9	7.9	8.0	8.0	8.0	8.1	8.1	8.2	8.2	8.2	8.2	8.2	8.4	8.6	8.8	12.0	14.3	15.2	15.2	15.6	15.9	17.4	17.5	19.0	19.3	19.6
	342	327	341	327	352	547	335	500	346	382	352	287	354	310	410	131	238	243	245	245	246	297	299	309	300	299
	12	11	8	H	13	G	1	8	13	u	13	13	13	1	13	1	1	1	11	11	11	11	1	1	H	4
	090387	070269	Q9MD83	070271	091855	045965	062853	Q9ZZQ2	Q9PUA9	Q9XUK8	Q91856	Q9PT44	6XLA60	Z00W60	QUPW33	Q9JKE8	Q9JKA3	Q9JKA2	Q9JKA4	Q9JKA1	Q9JKA0	Q9JKT3	QUIKUU	Q9JKT8	Q9JKT4	Q9NYW5
	090387 kaposi's sa		ç	0/02/1 10/00/10			Conord total	Section States California Communication Comm	tiode orna certain	Q9xuxo caenotiabut							1 100				i u					homo

## ALIGNMENTS

	AEFSVPLLIFLFAVLLLIFSLGRHTROMRNTVAGSRVPGRGAPISALLSILSFLILYFSH 240	AEFSV	181	Db
		AEFSV	181	Qy
	RISKLVPWMILGSLLYVSMICVFHSKYAGFWVPYFLRKFFSQNATIQKEDTLAIQIFSFV 180	RISKL	121	дb
		RISKL	121	Qγ
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		FIFYV	61	Qy
	MLESHLIIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQL 60	MLESHI	1	망
		MLESHI	1	Qy
0;	ν	299;	Best Loc Matches	<b>~</b> m
	100.0%; Score 1521; DB 4; Length 299;	tch		^
	299 AA; 34333 MW; CFB17DD15645392C CRC64;	•	Receptor. SEQUENCE	SQ
	EMBL; AF227129; AAF43902.1;	AF227	EMBL;	DR
	Cell 100:693-702(2000).	100:69	Cell	RL
	"A novel family of mammalian taste receptors.";	"A novel far	"A no	짐꽃
	1	, ii	Adler E.,	RA
	M.A. Chandrachokar T. Ruba N.J.P.	SEQUENCE FROM N.A.	SEQUE	RP
		[1]	[1] NCB1	R C
	Mammalia; Eutheria; Primates; Catarrilli; nominicae; "C"C".	lia; E	Mamma	8
	hordata;	yota;	Eukar	88
	CANDIDATE TASTE RECEPTOR 1281.	DATE T	CANDI	DE
	TremBirel. 15, Last annotation update)	01-OCT-2000	01-00	DI.
	(TrEMBLrel. 15, Created) (TrEMBLrel. 15, Last sequence update)	01-OCT-2000 01-OCT-2000	01-00	3 5
		7;	Q9NYW7	AC
	PRELIMINARY; PRT; 299 AA.	7	Q9NYW7	ID Q
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Indels

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Best Local Similarity
Matches 154; Conserv
                                                                                                                                                                                                                                              Q9JKU1 PRELIMINARY; PRT; 335 AA.
Q9JKU1;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
Q1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
CANDIDATE TASTE RECEPTOR T2R1.
                                                                                        SEQUENCE FROM N.A. Adler E., Hoon M.A.,
Adler E., Hoon M.A., Mueller C.S., zuker C.S., novel family of mammalian Cell 100:693-702(2000).
                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor.
SEQUENCE
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OSJKT2;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation updat
CANDIDATE TASTE RECEPTOR T2R19.
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Zuker C.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A novel family of mammalian taste Cell 100:693-702(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF227149; AAF43922.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                        K.L.,
                                                taste
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Pred. No. 1.2e-46;
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                           receptors.";
                                                                                           Chandrashekar
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; Murinae; Rat
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; Murinae; Mus
                                                                                      Ryba
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Best Local Similarity 36.4
Matches 114; Conservative
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Best Local Similarity
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"A novel family of mammalian tas Cell 100:693-702(2000).
EMBL; AF227130; AAF43903.1; -. Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-OCT-2000 (TrEMBLrel. 15, Last annotation
CANDIDATE TASTE RECEPTOR T2R3.
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                                        184
                                                                                      169
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                                                                                                                                                                       MRISKLVPWMILGSLLY------VSMICVFHSKYAGFMVPYFLRKFFSQNATIQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hoon M.A., Mueller K.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                316 AA;
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                                 ----WYLPPLIVSLASYSLLIFSLGRHTRQMLQNGTSSRDPTTEAHKRAIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35914 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                 26.6%; Score 405; DB 4; 36.4%; Pred. No. 8.1e-21; tive 43; Mismatches 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.4%; Score 767; DB 11; 51.8%; Pred. No. 1.3e-45; tive 53; Mismatches 87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chandrashekar J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              316
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                                                                                                                                                                                                                                                                                                                                                                                                                      114; Indels
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Euteleostomi;

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SILSF---LILYFSHCMIKVFLSSL-KFHIRRFIFLFFILVIGIYPSGHSLILILGNPKL

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RESULT
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Q9NYM3
AC Q9NYM3
AC Q0
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Matches 101
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01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-OCT-2000 (TrEMBLrel. 15, Last annotation
CANDIDATE TASTE RECEPTOR T2R8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9NYW2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A novel family of mammalian taste Cell 100:693-702(2000). EMBL; AF227134; AAF43907.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adler E., E
Zuker C.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
01-OCT-2000 (TrEMBLrel. 15, Cast annotation update)
CANDIDATE TASTE RECEPTOR T2R7.
                                                                                                                                                                                                                                                                                                                          Q9NYW3
                                                                                                                                                                                                                                                                                 Q9NYW3;
                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KQT---FVVMLRC 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KQNAKKFLLHSKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DMVVHWILLGCFAISLLVSLIAAIVLSCDYRFHAIAKHKRNITEMFHVSKIPYF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SKLVPWMILGSL---LYVSMICV-----FHS-----KYAGFMVPYFLRKFFS 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IVIFFIEFIMCSANCAILL-----FINELELWLATWIGVFYCAKVASVRHPLFIWLKMRI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APISALLSILSFLILYFSHCMIKVFLSSLKFHIRRFIFL-----FFILVIGIYPSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSLILILGNPKLKQNAKKFL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSLILIVLNNKLROTFVRML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hoon M.A., Mueller K.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPLTLFNLFAI-----VPFIVSLISFFLLVRSLWRHTKQIKLYATGSRDPSTE 228
                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 376; DB 4
Pred. No. 7.7e-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5E3D94B726A52413
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                                                                                                                                                                                                                                                                                                                                 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB .4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ryba N.J
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Best Local Similarity
Matches 100; Conserv
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SEQUENCE FROM N.A.
Adler E., Hoon M.A., Mueller K.L.,
Zuker C.S.;
PA novel family of mammalian taste
Cell 10:693-702(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF227133; AAF43906.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                           QNYW1;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-OCT-2000 (TrEMBLrel. 15, Last annotation
CANDIDATE TASTE RECEPTOR T2R9.
                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                          Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                               Q9NYW1
                                                                                                                                                                            "A novel family of mammalian taste receptors."; Cell 100:693-702(2000).
EMBL; AF227135; AAF43908.1; -.
                                                                                                                                                                                                           Adler E., E
Zuker C.S.;
                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                      132
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                               247 YYLSFLIATSSYFMPETELAVIFGESIALIYPSSHSFILILGNNKLRHASLKVI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 WMILGSLLYVSMICVFHSKYA-----GFMVPYFLRKFFSQNATIQKEDTLAIQIFSF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 LAVIQFLLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQLFIFYVNVIVIF
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                                                                                                                                                                                                                                                                                                                                                                                                             HCMIKVFLSSLKFHIRRFIFLFFILVIG-IYPSGHSLILILGNPKLKQNAKKFL
                                                                IYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQLFI----F 63
                                             YVNVIVIFFIEFIMCSANCAILLFINELELWLATWLGVFYCAKVASVRHPLFIWLKMRIS 123
FMLLFPGTYGNSVLVSIVNVVWTFANNSSLWFTSCLSIFYLLKIANISHPFFFWLKLKIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 32.7
96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hoon M.A., Mueller K.L., Chandrashekar J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318 AA;
                                                                                                                                                                                                                       Hoon M.A.,
                                                                                                                                                           312
                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                           A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36549 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.7%; Score 376; DB 4; 32.7%; Pred. No. 7.9e-19;
                                                                                                                                                            35611 MW;
                                                                                                                   24.4%;
                                                                                                                                                                                                                         Mueller K.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60;
                                                                                                          60;
                                                                                                                     Score 371.5; DB Pred. No. 1.6e-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F187ADB2D8274B8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 120;
                                                                                                                                                             CCE66F1E31051F49
                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptors.";
                                                                                                                                                                                                                         Chandrashekar
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                                                                                                                                DB 4;
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                                                                                                                                   312;
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                                                                                                               Gaps
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RESULT
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Best Local Similarity
Matches 104; Conserv
O9NYWO PRELIMINARY;
O9NYWO;
O1-OCT-2000 (TremBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9JKE9 PRELIMINARY: PRT; 297 AA. Q9JKE9; 01-OCT-2000 (TrEMBLrel. 15, Created) 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-OCT-2000 (TrEMBLrel. 15, Last annotation update) TASTE RECEPTOR RT2R6 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                    285
                                                                                                          292
                                                                                                                                                                                                                                                                                                                                                                                                                                       NON
                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A novel family of mammalian taste receptors."; Cell 100:693-702(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                              173
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                                                                                                                                  225
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                                                                                                                                          FLILYFSHCMIKVFLSSLKFHIR-RFIFLFFILVIGIYPSGHSLILILGNPKLKQNAKKF 291
                                                                                                                                                                        LVMLF----PFSVSLVSF----LLLILSLWRHTRQMQLNVTGYNDPSTTAHVKATKAVIS
                                                                                                                                                                                      AIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTROMRNTVAGSRVPGRGAPISALLSILS : : | | | | | : | :::|
                                                                                    LCRVK 289
                                                                                                          LLHSK
                                                                                                                             FLVLFIVYCLAFLIATSSYFMPESELAVIWGELIALIYPSSHSFILILGNSKLKQASVRV
                                                                                                                                                                                                                    L--ILSLC-----FSLPVTENLADDFRRCVKTKERINSTLRCKLNKAGYASVKVNLN
                                                                                                                                                                                                                                                                                CSANCAILLFI----NELELWLATWLGVFYCAKVASVRHPLFIWLKNRISKLVPWMILGS 133
                                                                                                                                                                                                                                          LLYVSMICVFHSKYAGFMVPY------FLRKFFSQ----NATIQ------KEDTL
                                                                                                                                                                                                                                                                 RGKEMRIIDEFWTLTNHLSVWFATCLSIFYFFKIANFFHPLFLWIKWRIDKLILRTLLAC 122
                                                                                                                                                                                                                                                                                                              LVGILGNAFIALVNFMGWMKNRKITAIDLILSSLAMSRICLQCIILLDCIILVQYPDTYN
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                                                                                                          296
                                                                                                                                                                                                                                                                                                                                                                                                                        1 1
297 AA; 34107 MW;
                                                                                                                                                                                                                                                                                                                                                           24.3%; Score 369; DB 11;
ilarity 34.1%; Pred. No. 2.2e-18;
Conservative 51; Mismatches 106;
                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mueller K.L.,
  15,
  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                       873D0440C2863E25 CRC64;
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                                                                                                                                                                                                                                                                                                                                                              44;
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  Query Match
Best Local S
Matches 97
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EMBL; AF227137; AAF43910.1; -.
Receptor.
SEQUENCE 303 **
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Best Local Similarity 31.0
                                                                                                                                                                                                                           Q9NYV9 PRELIMINARY; PRT; 303 AA.
Q9NYV9;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
CANDIDATE TASTE RECEPTOR T2R13.
                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                             Adler E., Hoon M.A.,
Zuker C.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor.
SEQUENCE
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01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
CANDIDATE TASTE RECEPTOR T2R10.
Homo sapiens (Human).
Elkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                              NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A novel family of mammalian taste Cell 100:693-702(2000).
EMBL; AF227136; AAF43909.1; -.
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                                                                                                                                                                                                                                                                                                                                                            RVLQQLKCCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --FVAEFSVPL-LIFLEAV-----LLLIFSLGRHTRQMRNTVAGSRVPGRGAPISALLSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RTNMVLPFMIV--FLLISSLLNF-----AYIAKILNDYKT--KNDTVWDLNMYKS
                                                                                                                                                                                                                                                                                                                                                                                                       ISFIILFILYFIGMAIEISCFTVRENKLLLMFGMTTTAIYPWGHSFILILGNSKLKQASL 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RISKLVPWMILGSLLYVSMICVFHSKYAGFMVPYFLRKFFSQNATIQKEDTL-AIQIFS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FIQIFSPNIYASGN--LIEYISYFWVIGNQSSMWFATSLSIFYFLKIANFSNYIFLWLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IVIFFIEFIMCSANCAILLFI-----NELELWLATWLGVFYCAKVASVRHPLFIWLKM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
23.4%; Score 356; DB 4; 31.9%; Pred. No. 1.8e-17; tive 69; Mismatches 116
                                                                                                                                        Mueller K.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35365 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.5%;
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                                                                                                                 taste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 358; DB 4;
Pred. No. 1.3e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K.L.,
                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                               756BF5382E36BFB5
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                                                                                                              receptors
                                                                                                                                         Chandrashekar
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                        Length 303;
                                                              CRC64;
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97; Conservative

Indels

22;

Gaps

11;

286 QNAKKFLL

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Matches
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01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
TASTE RECEPTOR RT2R12.
                                                                                                                                                                                                                                                                                                                                 Adler E., Hoon M.A., Mueller K.L., zuker C.S.;
"A novel family of mammalian taste Cell 100:693-702(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9JKE7
                                                                                                                                                                                                                                                                                                                        EMBL; AF240768; AAF45306.1;
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
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                                                                                            120 LWLKWRFPALVPWLLLGSIL-VSFIVTLMFFWGNHTVYQA-----FLRRKFSGNTTF-KE
                                                                                                                    116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EILVSWFLALHYLAIFVSGTGLRIMIFSWIVSNHFNLWLATIFSIFYLLKIASFSSPAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FIFYVNVIVIFFIEFIMCSANCAILLF----INELELWLATWLGVFYCAKVASVRHPLFI 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLILY--FSHCMIKVFLSSLKFHIRRFIFLFFILVIGIY-PSGHSLILILGNPKLKQNAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YLKWRVNKVILMILLGTLVFLFLNLIQINMHIK--DWLDRY--ERNTTWNFSMSDFETFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLLFYASFFLCVLISWISEL---YQNTVIYMLCETIGVFSPSSHSFLLILGNAKLRQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KELL
                                                                                                                                                                                                             MLESHLIIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQL 60
            ALLSILSFLILYFSHCMIKVFLSSLKFHIRRFIFLFFILVIGIYPSGHSLILLILGNPKLK 285
                                                                                                                                         CVGLVNSFYYSLHLVEYSRSLARQLISLHMDFLNSATFWFGTWLSVLFCIKIANFSHPAF 119
                                                                                                                                                                                        WIRRLEIDYFMPLKLVTTSIPCSLFLVSILLLINSLRRHSQRMQHNAHSLQDPNTQAHSR
                                                                    DTLAIQIESE----VAEFSVPLLIFLEAVLLLIFSLGRHTRQMRNTVAGSRVPGRGAPIS
                                                                                                         IWLKMRISKLVPWMILGSLLYVSMICVF-----HSKYAGFMVPYFLRKFFSQNATIQKE 169
                                                                                                                                                              FIFYVNVIV--IFFIEFIMCSANCAILL---FINELELWLATWLGVFYCAKVASVRHPLF 115
308 AA;
                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                   36009 MW;
                                                                                                                                                                                                                                      23.4%; Score 355.5; DB 11; Length 31.8%; Pred. No. 1.9e-17; tive 56; Mismatches 131; Indels
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Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                        Chandrashekar
                                                                                                                                                                                                                                                                                                                                                receptors.";
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Matches 98
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01-OCT-2000 (TrEMBLrel. 15, Last sequence up

01-OCT-2000 (TrEMBLrel. 15, Last annotation

01-OCT-2000 (TrEMBLrel. 15, Last annotation

CANDIDATE TASTE RECEPTOR T2R8.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                          09JKT7,
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence up
01-0CT-2000 (TrEMBLrel. 15, Last annotation
CANDIDATE TASTE RECEPTOR T2R7.
Rattus norvegicus (Rat)
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Zuker C.S.;
                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
NCBI_TaxID=10116;
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                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9ЈКТ7
Adler E., Hoon M.A., Zuker C.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 WLKMRISKLYPWMILGSLLYVSMICVFHSKYAGFMVPYFLRKFFSQNATIQKEDTLAIQI 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMVSFLLLYTSY-----FLSLLISWIAQKHHSKLVDIIGIITELMYPSVHSFILILGNSK
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                                                 Ryba N.J.P.,
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Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9JKT9 PRELIMINARY; PRT; 308 AA. Q9JKT9; 01-OCT-2000 (TrEMBLrel. 15, Created) 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-OCT-2000 (TrEMBLrel. 15, Last annotation update) CANDIDATE TASTE RECEPTOR T2R4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A novel family of mammalian taste Cell 100:693-702(2000). EMBL; AF227142; AAF43915.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adler E., H
Zuker C.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat)
ŗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-10116;
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                                           179
                                                                             128 --VVFIFLSGCLLTSWLLCFPQFSKMLNNSKMYWGNTSWLQQQKNVFLINQSLTNLGIFF
                                                                                                                                        124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 MIMESVTPETVALVSFILLIESLWKHLQKMHLSSRGERDPSTKAHVNALRIMVSELLLYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 VAEFSV-PLLIFLEAVLLLIFSLGRHTROMRNTVAGSRVPGRGAPISALLSILSFLILYF
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       KLVPWMILGSLLYVSMICVF--HSKYAGFMVPYFLRKFFSQ---NATIQKEDTLAIQIFS 178
                                                                                                                                                                            QVFF-PHILTEGNITEYITYIWVFLNHLSVWFATNLNILYFLKIANFSNSVFLWLKSRVR
                                                                                                                                                                                                        VIFFIEFIMCSANCA-----ILLFINELELMLATWLGVFYCAKVASVRHPLFIWLKMRIS 123
                                                                                                                                                                                                                                                                 LLAVI--QFLLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQLFIFYVNVI 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RISKLVPWMILGSLLYVSM-ICVFHSKYAGFMVPYFLRKFFSQNATIQKEDTLAIQIFSF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVKKVLLLILLGNLIFLMFNILQINTHIEDWMDQY--KRNITWDSRVNEFVGFSNLVLLE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AWLKYMKYSFSYLAGTELRVMMLTWVVSNHFSLWLATILSIFYLLKIASFSRPVFLYLKW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FYVNVIVIFFIEFIMCSANCAILLFI--NELELWLATWLGVFYCAKVASVRHPLFIWLKM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 28.7
86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hoon M.A., Mueller K.L., Chandrashekar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         308 AA; 35052 MW;
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                                                                                                                                                                                                                                                                                                                                                                                  61;
                                                                                                                                                                                                                                                                                                                                                                           Score 317.5; DB 11; Lengtl
Pred. No. 7.8e-15;
1; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rat
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Best Local Similarity
Matches 91; Conserv
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Q9JKT5;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
CANDIDATE TASTE RECEPTOR T2R9.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
CDI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adler E., Hoon M.A., Mueller K.L., Chandrashekar Zuker C.S.;
"A novel family of mammalian taste receptors.";
Cell 100:693-702(2000).
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      282
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                                                            GNPKLKQNAKKFL 292
                                                                                                                                                                          GAPISALLSILSFLILYFSHCM-IKVFLSSLKFHIRRFIFLFFILVIGIYPSGHSLILIL
                                                                                                                                                                                                                                             TSNYVL----INIGVISL-----LIMTLTACFLLIISLWKHSROMQSNVSGFRDLNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MLSAAEGILLSIATVEAGLGVLGNTFIALVNCMDWAKNKKLSKIGFLLFGLATSRIFIVW
TNSQLKQAFVKVL
                                                                                                                     EAHVKAIKFLISFIILFILYFIGVAVEIICMFIPENKLLFIFGLTTASVYPCCHSVILIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.8%; Score 317; DB 11; 29.1%; Pred. No. 8.5e-15; tive 61; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0FCE43EB9D3F0090 CRC64;
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INTERNISSA, SSP. LAMARCKII, SSP. SSP.
MACEDONICA, SSP. MEDA, SSP. MONTICOLA,
SSP. SAHARIENSIS, SSP. SCUTELLATA AND
SSP. SICULA).
V-> M (IN HAPLOTYPE 9).
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Gene 162:331-332(1995)
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"The deduced amino-acid sequence of opsin
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, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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032368; PubMed-7557454;
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(Rel. 34, Last sequence (Rel. 38, Last annotation)
                                                                                                                                                                                                                                                                                                                                              Retinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                   Lipoprotein;
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38, Last annotation updat
                                                                                                                                                                                                                                                                                                                                         protein;
3 (POTENTIAL).
CYTOPLASMIC.
4 (POTENTIAL).
EXTRACELLULAR.
5 (POTENTIAL).
CYTOPLASMIC.
6 (POTENTIAL).
EXTRACELLULAR.
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                                                                                                                                                           1 (POTENTIAL).
CYTOPLASMIC.
2 (POTENTIAL).
EXTRACELLULAR.
3 (POTENTIAL).
                                                                                                                                                                                                                                                                      EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                   Palmitate;
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                                                                                                                                                                                                                                                                                                                                    Transmembrane;
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PHOTORECEPTOR CELLS WHICH MEDIATES
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                                                                                                                                                                                                                                                                                                                   G-protein
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                                                                                                                                                                                                                                                                                                            Glycoprotein; Vision, tein coupled receptor;
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DOMAIN
MOD_RES
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CARBOHYD
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MOD_RES
SEQUENCE
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01-FEB-1991
15-JUL-1999
                                                                                                                                                                                                      Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Caprinae; Ovis.
                                                                  SEQUENCE OF 1-111 AND 144-239.
MEDLINE=83282605; PubMed=6224479;
Brett M., Findlay J.B.C.;
"Isolation and characterization of the CNBr proteolytically derived N-terminal fragment Biochem. J. 211:661-670(1983).
                                                                                                                                                                                                                                                                 RHODOPSIN
            MEDLINE-82013638; PubMed-7278988; Findlay J.B.C., Brett M., Pappin "Primary structure of C-terminal"
                                                                                                                                                           Pappin D.J.C.,
"A structural m
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                                                                                                                                                                                 SEQUENCE
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 "Primary structure rhodopsin.";
                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LFIFYVNVIVIFFIEFIMCSANCAILLFI----NELELW----LATWLGVFYCAKVASVR 111
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                                                                                                                                                D.J.C., Elipoulos E., Brett M., Findlay ctural model for ovine rhodopsin."; Biol. Macromol. 6:73-76(1984).
                                              OF 240-348.
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(Rel. 17, Last sequence up
(Rel. 38, Last annotation
                                                                                                                                                                                                                                                                                                                        STANDARD;
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21.8%;
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CYTOPLASMIC.
ACETYLATION (BY SIMILARITY).
N-LINKED (GLCNAC...) (BY SIN
N-LINKED (GLCNAC...) (BY SIN
RETINAL CHROMOPHORE.
PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY GOGORDON (BY RK) (BY SIMILARITY).
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              D.J.C.; functional
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on update)
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Best Local S
Matches 69
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"Sequence variability in the retinal-attachment domain of mammalian "sequence variability in the retinal-attachment domain attachment domai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RETINAL BINDING S MEDLINE-84178280;
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[4]
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PRINTS; PR00238; OPSIN.
PRINTS; PR00579; RHODOPSIN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS00238; OPSIN; 1.
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DOMAIN
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TRANSMEM
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TRANSMEM
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                                                                                                                                                                                                                                                                                      DISULFID
MOD_RES
SEQUENCE
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SUBCELLULAR LOCATION: INTEGRAL
TISSUE SPECIFICITY: ROD SHAPED
VISION IN DIM LIGHT.
                                                                  88
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                                                                                                LFIFYVNVIVIFFIEFINCSANCAILLFI----NELELW----LATWLGVFYCAKVASVR 111
                                                                                                                                    MLAAYM---FLLIVLGFPINFLTLYVTV-
                                                                FGGFTTTLYTSLHGYFVFGPTGCNLEGFFATLGGEIALWSLVVLAIERYVVVCKPMSNFR
FGENHAIMGVAFTWVMALACAAPPLVGW--
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                                                                                                                                                                                                     Similarity 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR000276; -.; IPR000732; -.;
                                -HPL----FIW----LKMRISKLVPWMILGSLLYVSMICVFHSKYAGFMVPYFLR---
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21.1%;
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N-LINKED (GLCNAC...) (BY SIN
RETINAL CHROMOPHORE.
PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
PHOSPHORYLATION (BY RK) (BY S)
PHOSPHORYLATION (BY CRC64;
                                                                                                                                                                                                         62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 (POTENTIAL).
EXTRACELLULAR.
7 (POTENTIAL)
                                                                                                                                                                                                       Score 129.5; l
Pred. No. 0.02:
52; Mismatches
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EXTRACELLULAR.
5 (POTENTIAL).
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CYTOPLASMIC.
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PHOTORECEPTOR CEI
                                                                                                                                        ·----QHKKLRTPLNYILLNLAVADLFMV
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SIMILARITY).
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                                                                                                                                                                                                                                                                                                                           PhosphoryIstion; I
DOMAIN 1
TRANSMEM 37
DOMAIN 62
TRANSMEM 74
DOMAIN 99
DOMAIN
                                                                          PRINTS: PR00237; GPCRHODDPSN.
PRINTS: PR00238; OPSIN.
PRINTS: PR00579; RHODOPSIN.
PROSITE: PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE: PS50262; G_PROTEIN_RECEP_F1_2;
PROSITE: PS00238; OPSIN; 1.
                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                      INTERPRO; IPRO00276; -.
INTERPRO; IPRO00732; -.
INTERPRO; IPRO01760; -.
PFAM; PF00001; 7tm_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P79863;
01-NOV-1997
01-NOV-1997
30-MAY-2000
                                                                                                                                                                               EMBL; U81514; AAC60251.1; GCRDB; GCR_1485; -.
                                                                     Photoreceptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAJER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Raja erinacea (Little skate).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-RETINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rajiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPSD_RAJER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 158
                                                                                                                                                                                                                                                                                           BE PHOSPHORYLATED.
MISCELLANEOUS: THIS RHODOPSIN HAS AN ABSORPTION MAXIMA SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RIOPSIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GHSLILILGNPKLKQNAKKFLLHSKCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RVPGRGAPISALLSILSFLILYFSHCMIKVFLSSLKFHIRRFIFL----FFILVIGIYPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -- KFFSQNATIQKEDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -NPVIYIMMNKQF----RNCMLTTLCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rajidae;
                                                                 Retinal protein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                        Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35,
39,
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61
73
98
113
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Last sequence up
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      1 (POTENTIAL).
CYTOPLASMIC.
2 (POTENTIAL).
EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                            opsin cDNA from the skate retina.";
                                             : Palmitate; G-protein EXTRACELLULAR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                    ð
                                                              Glycoprotein; Vision;
                                                                                                                                                                                                                                                                                                                                                  CELLS
                                                      coupled
                                                                                                                                                                                                                                                                                                                                                                               OPSIN,
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                                                     receptor
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Best Local
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P28681;
01-DEC-1992
01-DEC-1992
15-JUL-1999
Gale J.M., Tobey R.A., D'Anna A.;

"Localization and DNA sequence of a replication rhodopsin gene locus of Chinese hamster cells.";

J. Mol. Biol. 224:343-358(1992).

-i- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSO MEDIATE VISION. THEY CONSIST OF AN APOPROTEI LINKED TO CIS-RETINAL.

-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROT-

-i- TISSUE SPECIFICITY: ROD SHAPED PHOTORECEPTOR
                                                                                                                                              Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                     RHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
TRANSMEM
DOMAIN
                                                                                               MEDLINE~92219256; PubMed-1560457;
                                                                                                            TISSUE-OVARY;
                                                                                                                     SEQUENCE FROM
                                                                                                                                          Cricetulus.
                                                                                                                                                                                               RHODOPSIN
                                                                                                                                                                                                                                                             CRIGR
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SEQUENCE
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BINDING
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                                                                                                                                                                                                                                                                                                     AVYNPLIYILMNKQFR
                                                                                                                                                                                                                                                                                                                         ---HSLILILGNPKLK 285
                                                                                                                                                                                                                                                                                                                                                                                                                                           ----FIWLKMRIS----KLVPWMILGSLLYVSMICVFHSKYAGFWVPYFLR-----KFFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VIVIFFIEFIMCSANCAILLFI----NELELWLATWLGV----FYCAKVASVR----HPL 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MFFLI-----LTGLPVNFLTLFVT----IQHKKLRQPLNYILLNLAVSDLFMVFGGFTTT
                                                                                                                                                                                                                                                                                                                                           VTRMVIIMVVAELICWVPY-----ASVAF----YIFINQGCDFTPFFMTVPAFFAKSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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2 (Rel. 24,
3 (Rel. 38,
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Last
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                                                                                                                                                                                                                 sequence update)
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CYTOPLASMIC.
N-LINKED (GLCNAC. . .) (POTE
N-LINKED (GLCNAC. . .) (POTE
RETINAL CHROMOPHORE (BY SIMI
PALMITATE (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 (POTENTIAL).
CYTOPLASMIC.
4 (POTENTIAL).
EXTRACELLULAR.
5 (POTENTIAL).
CYTOPLASMIC.
6 (POTENTIAL).
EXTRACELLULAR.
7 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 129.5;
Pred. No. 0.
                                                                                                                                                                                                                                                 PRT;
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           MEMBRANE PROTEIN
 PHOTORECEPTOR
                             HE LIGHT-ABSORBING AN APOPROTEIN, OPS
                                                                                                                                                                                                                                                 348
                                                                                                                                                                                                     update)
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                                                                       origin
CELLS
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() (POTENTIAL).
(BY SIMILARITY).
                              OPSIN, COVALENTLY
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WHICH
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MEDIATES
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Best Local
                                                                                                                                   Matches
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PRINTS; PRO0238; OPSIN.
PRINTS; PR00579; RHODOPSIN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS00238; OPSIN; 1.
PROSITE; PS00238; OPSIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
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                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
DISULFID
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERPRO; IPR001760; -. PFAM; PF00001; 7tm_1; 1
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                                                                                                                                                                                       LIPID
MOD_RES
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acetylation.
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                                                                                                           MLESHLIIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKM-APLDLLLSCLAVSRIFLQ 59
                                                                                      MLAAYM---FLLIVLGFPINFLTLYVTV-----QHKKLRTPLNYILLNLAVADLFMV
 FGENHAIMGVVFTWI-MALACAAP-PLVGWSRYIPEGMQCSCGVDY----YTLKPEVN
                     ----HPL----FIWLKMRISKLVPWMILGSLLYV--SMICVFHSKYAGFMVPYFLRKFFS 161
                                                               LFIFYVNVIVIFFIEFIMCSANCAILLFI----NELELW----LATWLGVFYCAKVASVR 111
                                           FGGFTTTLYTSLHGYFVFGFTGCNLEGFFATLGGEIALWSLVVLAIERYVVICKPMSNFR
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                                                                                                                                   Similarity 21.070; Conservative
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348 AA;
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                                                                                                                                                                                          MW;
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N-LINKED (GLCNAC...
BY SIMILARITY.
RETINAL CHROMOPHORE.
                                                                                                                                             Score 128.5; DE Pred. No. 0.027;
                                                                                                                                                                                         PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
PHOSPHORYLATION (BY RK) (BY SIMILARITY).
A5CDF27804F30AA1 CRC64;
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CYTOPLASMIC.
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3 (POTENTIAL).
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CYTOPLASMIC.
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5 (POTENTIAL).
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                                                                                                                                                         DB 1;
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INTERPRO; IPRO00732;
INTERPRO; IPRO01760;
IPROM; PF00001; 7tm_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-SPRAGUE-DAWLEY; TISSUE-RETINAL MEDLINE-95383121; PubMed-7654522; Barnstable C.J., Morabito M.A.; "Isolation and coding sequence of the J. Mol. Neurosci. 5:207-209(1994).
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                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (DEC-1994) to the EM-
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PRINTS; PR00238; OPSIN.
PRINTS; PR00579; RHODOPSIN.
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GCRDB; GCR_1458;
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  Photoreceptor;
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: ROD SHAPED PHOTORECEPTOR CELLS WHICH MEDIATES VISION IN DIM LIGHT.
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                      PS00237; G_PROTEIN_RECEP_F1_1; 1. PS50262; G_PROTEIN_RECEP_F1_2; 1. PS00238; OPSIN; 1.
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    protein;
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         Transmembrane;
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                                                     Anura; Neobatrachia; Bufonoidea;
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ACETYLATION (BY SIMILARITY),
N-LINKED (GLCNAC. . .) (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (BY SIMILARITY).
RETINAL CHROMOPHORE.
PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
BY SIMILARITY).
                                                                Craniata; Vertebrata; Euteleostomi;
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2 (POTENTIAL).

EXTRACELLULAR.

3 (POTENTIAL).
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the European Bioinformatics Institute. The
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-I- FUNCTION: VISUAL PICKENTS ARE THE LIGHT-ABSORBING MOLECULES THAT MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY LINKED TO CIS-RETINAL. THIS RECEPTOR IS COUPLED TO THE ACTIVATION OF PHOSPHOLIPASE C.
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Smith W.C.;
       93
                                                             37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Rhodopsins from three frog and toad species: sequences and functional comparisons.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98288405; PubMed-9533857;
                                                                                         9
VTMYSSMNGYFILGATGCYVEGFFATLGGEIALWSLVVLAIERYVVVCKPMSNFRFSENH
                         VNVIVIFFIEFIMCSANCAILLFI----NELELW----LATWLGVFYCAKVASVR----H 112
                                                    YSILCAYMELLILLGEPINEMTLYVT----IQHKKLRTPLNYILLNLAFANHEMVLCGET
                                                                              YFLLAVIQF---LLGIFTNGIIVVVNGIDLIKHRKM-APLDLLLSCLAVSRIFLQLFIFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES
BE PHOSPHORYLATED (BY SIMILARITY).
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPSIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCR_2484;
                                                                                                                  Conservative
                                                                                                                                                                                        354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Retinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Donner K., Hargrave P.A., McDowell J.H., Popp
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15
296
322
323
323
187
39777
                                                                                                                              8.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein;
                                                                                                                                                                                     ¥₩;
                                                                                                                 57;
                                                                                                                                                                              7 (POTENTIAL).

CYTOPLASMIC.

N-LINKED (GLCNAC. . .) (BY S
N-LINKED (GLCNAC. . .) (BY S
N-LINKED (GLCNAC. . .) (BY S
RETINAL CHROMOPHORE.
PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
                                                                                                            Score 128.5; DB 1;
Pred. No. 0.027;
7; Mismatches 130;
                                                                                                                                                                                                                                                                                                                           2 (POTENTIAL)
EXTRACELLULAR
3 (POTENTIAL)
CYTOPLASMIC
4 (POTENTIAL)
EXTRACELLULAR
5 (POTENTIAL)
CYTOPLASMIC
6 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC.
2 (POTE:--
                                                                                                                                                                                                                                                                                                     6 (POTENTIAL).
EXTRACELLULAR.
7 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane; Glycoprotein; Vision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              There are no restri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein coupled receptor
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                                                                                                                                                                                                                                                     SIMILARITY)
                                                                                                                                         354;
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                                                                                                            55;
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-RROCCOG DT DT AC

RHODOPSIN

Gaps

16;

92 64

SEQUENCE FROM N.A.

Bufo.

15-JUL-1998 15-JUL-1998 30-MAY-2000

(Rel. (Rel. (Rel.

OPSD\_BUFBU P56514; BUFBU

STANDARD;

OPSD\_B

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RESULT
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062793;
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15-DEC-1998
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
Mammalia; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MESBI
                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted (MAR-1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RHODOPSIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113
                 TRANSMEM
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restrained the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mesoplodon
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                                                                                                PROSITE; PS00237;
PROSITE; PS50262;
PROSITE; PS00238;
                                                                                                                                                                    PFAM; PF00001;
                                                                                                                                                                                           INTERPRO; IPRO00276; INTERPRO; IPRO00732;
                                                                                                                                                                                                                  EMBL; AF055316; AAC12763.1; -.
                                                                                                                                                                                                                                       or send
                                                                                                                                                                                                                                                     entities
                                                                                                                                                                                                                                                              modified and this statement is not removed.
                                                                                                                                    PRINTS;
                                                                                                                                                         PRINTS;
                                                    DOMAIN
                                                                          Phosphorylation;
                                                                                                                                                                                INTERPRO; IPRO01760;
                                                             Acetylation.
                                                                                      Photoreceptor;
                                                                                                                                                                                                                                                                                                                                             LINKED TO CIS-RETINAL.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: ROD SHAPED PHOTORECEPTOR CELLS WH
VISION IN DIM LIGHT.
PPM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR
BE PHOSPHORYLATED (BY SIMILARITY).
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED
                                                                                                                                                                                                                                                                                                                                     OPSIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIATE VISION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLSILSFLILTESHCMIKVFLSSLKFHIRRFIFL----FFILVIGIYPSGHSLILILGNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PL----FIWLKMRISKLVPWMILGSLLYV--SMICVFHSKYAGFMVPYFLRKFFSQNATI
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                                                                                     PR00579; RHODOPSIN.
; PS00237; G_PROTEIN_RECEP_F1_1;
; PS050262; G_PROTEIN_RECEP_F1_2;
; PS00238; OPSIN; 1.
; Ceptor; Retinal protein; Transmer
                                                                                                                                                                                                                                       s requires a license agreement (S
an email to license@isb-sib.ch).
                                                                                                                                              PR00237; GPCRRHODOPSN.
PR00238; OPSIN.
                                                                                                                                                                                                                                                                           non-profit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eutheria;
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(Rel.
(Rel.
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ROBLINSON P.R.;
AR-1998) to the EMBL/GenBank/DDBJ databases.
AR-1998) to the EMBL/GenBank/DDBJ databases.
It VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT IN VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
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37
62
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37,
38,
                                                                            Lipoprotein;
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         36
61
73
98
113
                                                                                                                                                                                                                                                                           institutions as long
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       EXTRACELLULAR.

1 (POTENTIAL).

CYTOPLASMIC.

2 (POTENTIAL).

EXTRACELLULAR.
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                                                                            Palmitate; G-protein
                                                                                         Transmembrane;
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                                                                                                                                                                                                                                                      (See
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                                                                                                                                                                                                                                                      http://www.isb-sib.
                                                                                                                                                                                                                                                                 Usage
                                                                               Glycoprotein; Vision;
tein coupled receptor;
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                                                                                                                                                                                                                                                                                         restrictions
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Best Local
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DOMAIN
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DOMAIN
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.MOD_RES
SEQUENCE
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DISULFID
BINDING
LIPID
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                                                                                                                                          OPSD_TURTR
062798;
15-DEC-1998
15-DEC-1998
15-JUL-1999
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SEQUENCE FROM N.A.
MEDLINE-98129138; PubMed-9471225;
                                                                                                Eukaryota;
Mammalia;
                                                                                                                           RHO
                                                                                                                                  RHODOPSIN
                                                                                                                                                                                                                                                                                                 193
                                                                                                                                                                                                                                                                                                                  161
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                                                                                        Tursiops.
                                                                                                                Tursiops truncatus
                                                                                                                                                                                                                          306 YIMMNKQF----RNCMLTTLCC
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                                                                                                                                                                                                                                                                                                                                                                                                                       9 YFLLAVIQEL---LGIFTNGIIVVVNGIDLIKHRKM-APLDLLLSCLAVSRIFLQLFIFY
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                                                                                                                                                                                                                                                                                                                                                                                                                                         67; Conservative
                                                                                                Eutheria;
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                                                                                                          Metazoa;
                                                                                                                                            (Rel.
(Rel.
(Rel.
                                                                                                                                                                                STANDARD;
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37,
38,
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187
187
296
296
323
343
                                                                                                (Atlantic bottle-nosed dolphin).
; Chordata; Craniata; Vertebrata; Eutel.
; Cetartiodactyla; Cetacea; Odontoceti;
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EXTRACELLULAR.
5 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                             63;
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CYTOPLASMIC.
4 (POTENTIAL).
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7 (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC.
CYTOPLASMIC.
ACETYLATION (BY SIMILARITY).
ACETYLATION (BY SIMILARITY).
BY SIMILARITY).
BY SIMILARITY).
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6 (POTENTIAL).
EXTRACELLULAR.
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Pred. No. (
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PALMITATE (BY SIMILARITY).
PHOSPHORYLATION (BY RK) (BY F83010DC40C450D5 CRC64;
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RETINAL CHROMOPHORE
                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                              on update)
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                                             dolphin visual pigments.";
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                       OPSIN,
                                                                                                              Euteleostomi;
                       MOLECULES THAT SIN, COVALENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                348;
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                                                                                                     Delphinidae;
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Best Local S
Matches 64
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INTERPRO; IPR000276; -.
INTERPRO; IPR000732; -.
INTERPRO; IPR0007160; -.
PFAM; PF000001; 7tm.1; 1.
PFRINTS; PR00237; GPCRHODOPSN.
PRINTS; PR00238; OPSIN.
PRINTS; PR00238; OPSIN.
PRINTS; PR00579; RHODOPSIN.
PRINTS; PR00579; GPCRFOTEN_RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS00238; OPSIN; 1.
                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
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BINDING
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ACETYLATION (BY SIMILARITY).

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RETINAL CHROMOPHORE.

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PHOSPHORYLATION (BY RK) (BY SIMILARITY).
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No. 0.
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095371;
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Construction of an approximately 700 kb transcript map familial mediterranean fever locus on human chromosome 1 Genome Res. 9:1-21(1998).
-- FUNCTION: PUTATIVE ODORANT RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Centola M., Chen X., Sood R., Deng Z., Aksentijevich I., Bia Ricke D., Chen X., Wood G., Zaks N., Richards N., Krizman D. Mansfield E., Apostolou S., Liu J., Shafran N., Vedula A., H Cercek A., Kahan T., Gumucio D., Callen D.F., Richards R.I., Moyzis R.K., Doggett N.A., Collins F.S., Liu P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
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01-OCT-2000 (Rel. 40, Last
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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01-AUG-1988 (Rel
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Homo sapiens (Human).
'``rvota; Metazoa; Chordata;
'``rvia; Primates;
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VARIANTS ADRP.
MEDLINE-91051574;
                                                          MEDLINE-90136922; PubMed-2137202;
Dryja T.P., McGee T.L., Reichei E.,
Yandell D.W., Sandberg M.A., Berson
                                                                                                                                                                                             Bennett
                                                                                                                                                                                                                                       rhodopsin.";
                                                                                                                                                                                                                                                        Nathans J., Hogness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238
                                                                                                            "Rhodopsin mutations in autosomal Hum. Mutat. 2:249-255(1993).
                                                                                                                                  Al-Maghtheh M., Gregory Bhattacharya S.;
                                                                                                                                                    MEDLINE-94004905; PubMed-8401533;
                                                                                                                                                                                    Bennett J., Beller B., S
Submitted (NOV-1994) to
                                                                                                                                                                                                                                                                                                                                                                                                                                            295
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                    Nature
[5]
                                                                                           VARIANT ADRP HIS-23.
                                                                                                                                                               REVIEW ON ADRP VARIANTS
                                                                                                                                                                                                        SEQUENCE OF
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                                                "A point mutation
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MEDLINE=91015273; PubMed=2215617;
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Bashir R., Jay M.,
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Carballo M.;
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WEDLINE-95072600; PubMed-7981701;
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MEDLINE-93357759; Pu
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Fasick J.I., Robinson P.R.;
Fasick J.I., Robinson P.R.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
-i-FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MODEL OF THE PROPERTY OF AN APOPROTEIN, OPSI
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Mammalia; F
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Eukaryota; Metazoa; Chordata;
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WEDLING-95078913; PubMed-7987385;

Kumaramanickavel G., Maw M., Denton M.J.,
Orth U., Gehlmann R., Gal A.;

"Missense rhodopsin mutation in a family wast. Genet. 8:10-11(1994).
                                   MEDIATE VISION. THEY CONSIST OF AN APPOPROTEI
LINKED TO CIS-RETINAL.

1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROT
1- TISSUE SPECIFICITY: ROD SHAPED PHOTORECEPTOR
VISION IN DIM LIGHT.
1- PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SE
BE PHOSPHORYLATED (BY SIMILARITY).
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN
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Rosas D.J., Roman A.J., Weissbrod P., Macke J.P., Nathans "Autosomal dominant retinitis pigmentosa in a large family clinical and molecular genetic study.";
Chhrhalmol. Vis. Sci. 35:3134-3144(1994).
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Chordata; Craniata; Vertebrata; Euteleostomi;
Cetartiodactyla; Cetacea; Odontoceti; Delphin
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PRINTS; PR00238; OPSIN.
PRINTS; PR00579; RHODOPSIN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
PROSITE; PS00238; OPSIN; 1.
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                                               IIMVVAFLICWVPYASVAFYIFTHQGSDFGPIFMTIPSFFAKSSSIY---NPVIYIMMNK 311
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  KLKQNAKKFLLHSKCC 298
                                                                                            LLSILSFLILYFSHCMIKVFLSSLKFHIRRFIFL----FFILVIGIYPSGHSLILILGNP
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IPR000732;
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PALMITATE (BY SIMILARITY).

PHOSPHORYLATION (BY RK) (BY SIMILARITY).

70D8663DF7F59080 CRC64;
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7 (POTENTIAL)
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5 (POTENTIAL)
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3 (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 123; DB 1
Pred. No. 0.062;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122;
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SIMILARITY).
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RESULT 13
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Best Local S
Matches 71
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15-JUL-1998 (Rel. 36,
15-JUL-1999 (Rel. 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GP41_HUMAN O14843;
                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUTATIVE G PROTEIN-COUPLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A cluster of four occurring in close
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
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                                                                                                                       CARBOHYD
SEQUENCE
                                                                                                                                                                          DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                          PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                PFAM; PF00001; 7tm_1;
                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF024688; AAB86711.1;
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FLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQLFIFYVNVIV
                                                                                 Similarity
                                                                                                                                                                                                                                                                                                   coupled
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41
48
69
81
102
133
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179
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223
244
259
                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    George
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rge S.R., Nguyen
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Last annotation updat
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X
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                                                                                                                                                                                                                                                                                                      Transmembrane
                                                                                                                                                                           5 (POTENTIAL).
6 (POTENTIAL).
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                                                                                 Score 122.5; DE Pred. No. 0.067;
                                                                                                                         7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . ) (P
B3B19D62D11B6BA1 CRC64;
                                                                                                                                                         6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL)
                                                                                                                                                                                                                            CYTOPLASMIC
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1 (POTENTIAL).
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                                                                          Mismatches
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                                                                                                                                                                                                                               (POTENTIAL).
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                                                                           93;
                                                                                              Length 346;
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                                                                                                                                        (POTENTIAL)
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THE PROPERTY OF THE PROPERTY O
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PRINTS; PR00238; OPSIN.
PRINTS; PR00579; RHODOPSIN.
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS00238; OPSIN; 1.
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Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT
- MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
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O62794;
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Mammalia; Eutheria;
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: ROD SHAPED PHOTORECEPTOR CELLS WHICH MEDIAT VISION IN DIM LIGHT.
PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES M BE PHOSPHORYLATED (BY SIMILARITY).
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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MEDLINE-9747533; Pubmed-9335046;

A Petters R.M., Alexander C.A., Wells K.D., Collins E.B., Somme Petters R.M., Alexander C.A., Wells K.D., Collins E.B., Somme Blanton M.R., Rojas G., Hao Y., Flowers W.L., Banin E., Cideciyan A.V., Jacobson S.G., Wong F.;

T. "Genetically engineered large animal model for studying cone photoreceptor survival and degeneration in retinitis pigmento Nat. Blotechnol. 15:965-970(1997).

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C -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-1- TISSUE SPECIFICITY: ROD SHAPED PHOTORECEPTOR CELLS WHICH VISION IN DIM LIGHT.
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PRINTS; PR00579; RHODOPSIN.
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PROSITE; PS00238;
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BE PHOSPHORYLATED.

MISCELLANGOUS: THIS RHODOPSIN HAS AN ABSORPTION MAXIMA AT 495 N SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. OPSIN SUBFAMILY.
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FGENHAIMGLALTWVMALACAAPPLVGW------SRY----IPEGLQCSC 187
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Search completed: March 15, Job time: 1355 sec

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A;Title: The mitochondrial genome of the honeybee Apis mellifera: complete sequence A;Reference number: S52960; MUID:93114603
A;Accession: S52960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - honeybee mitochondrion C;Species: mitochondrion Apis mellifera (honeybee) A;Variety: ligustica C;Date: 28-0ct-1996 *sequence_revision 13-Mar-1997 *text_change 17-Mar-2000 C;Date: 28-0ct-1996 *sequence_revision 19-Mar-1997 *text_change 17-Mar-2000 C;Date: 28-0ct-1996 *sequence_revision 19-Mar-1997 *text_change 19-Mar-1997 *te
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-333 <CRO>
A;Cross-references: EMBL:L06178
C;Genetics:
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7.3	7.3	1.3		7.3	1.3	, ,	<b>'</b>	7.3	1.4	1	7.4	1.4	. (	7			7		1	7.5	:	7	
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Manual actif as of an acti	Nany dehydrogenase	probable NADH dehv	angiotensin II rec	and Torenami tr tee	and of the second of the	iodopsin homolog -	THOUGHT	whodonein - northe	Nanu dehydrogenase	glucose transport	OTIGOCOT LOCAPORT	olfactory recentor	hypothetical proce	quidiorenam in in icc	pariotoncin II rec	38.1K membrane pro	Hypothericat Proce	himsthatical prote	conserved hypothet	FIIOGOPO FII	rhodonein - Africa	probable iron-upta	

## ALIGNMENTS

A;Genome: mitochondrion
A;Genetic code: SGC4
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidoreductase В Ωy 밁 Q δÃ 밁 Qy В δÃ В Query Match 8.6%; Best Local Similarity 19.9%; Matches 67; Conservative 6 169 163 125 104 CAKVASVRHPLFIWLKM-RISKLVPWMILGSLLYVSMICVFHSKYAGFMVPYFLRKFFSQ 162 270 PSGHSLILILGNPKLKQN------AKKFLLHS 295 66 54 9 5 HLIIYELLAV------IQELLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAV 53 KKLLACSTIENSEYEIFILELNKNMEIAMIILYSENYELLISELNKENIQNENEMEYNK-NATIOKEDTLAIQIFSFVAE-----FSVPLLIFLFAVLLLIFSLGRHTROMRNTVAGSRV MSTLIKF-IPIYMMVSMTKINSWTLYFLITNSLYIS--------FYANKFYTL SSIFL-FFMIIVYLSSISFTKTDTFNFMVQMMFFLKIGTFPFHFWMIYSYEMMNWKQIFL SRIFLQLFIFYVNVIVIFFIEFIMCSANCAILLFIN----ELELW-----LATWLGVFY 103 HWFIXELITIFULMMUSUNIFIOMMLMEF--GTIISISLIN-IKSTNKTPSLIYYSVSVI 65 PGRGAPISALLSILSFLILYFSHCMIKVFLS-----SLKFHIRRFIFLFFILVIGIY 269 LMIWNYIIILKRVFLKMNFYKNNFIDDKDNKYMYHS 313 -----YQMYTFLTLMENYSMYPIFLSEVIKWNLIEMMVSVKAYNWILELLMISSM 277 63; Mismatches Score 131; DB 2; Length 333; Pred. No. 0.001; 130; Indels 76; Gaps 168 124 227 13;

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rhodopsin - sheep
(:Species: Ovis orientalis aries, Ovis ammon aries (domesti
C:Species: Paug-1982 #sequence_revision 30-eep-1990 #text_ch
C:Accession: A30407; A90319; A93264; A03155
R:Pappin, D.J.C.; Elipoulos, E.; Brett, M.; Findlay, J.B.C.
Int. J. Biol. Macromol. 6, 73-76, 1984
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JC4267; pc4072
R;Smith, W.C.; Martinko, J.M.; Wheeler, J.N.; Hargrave, P.A.; McDowell, J.H.
Gene 162, 331-332, 1995
A;Title: The deduced amino-acid sequence of opsin from rabbit rod photoreceptors.
A;Reference number: JC4267; MUID:96032368
A;Accession: JC4267
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A; Residues: 1-39:318-348 <SM2>
A; Residues: 1-39:318-348 <SM2>
A; Experimental source: rod photoreceptor cells
C; Comment: This protein is a component of rhodopsin together with the retinoid chromophe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;37-61/Domain: transmembrane #status predicted <TM1>F;75-99/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross·references: GB:U21688; NID:g710429; PIDN:AAA91640.1; A;Accession: PC4072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-348 <SMI>
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Best Local :
                                                                                                                                                                                                                  278
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                                                                                                                                                                                                                                                                                                                                                                                                       148
                                                                                                                                                                                                                                                                                                                       200 NESFV-----IYMFVVHFTIPLIIIFFCYGQLVFTVKEAAAQQQES-ATTQKAEKE
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                                                                                                                                                                                                             ILGNPKLKQNAKKFLLHSKCC
                                                                                                                                                                                                                                                    VTRMVIIMVIAFLICWVPYASVAFYIFTHQGSNFGPIFMTIPAFFAKSSSIY---NPVIY
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                                                                                                                                                                                                                                                                                                                                                                                          FGENHAIMGVAFTWI-MALACAAP-PLVGWSRYIPEGMQCSCGIDY----YTLKPEVN
                                                                                                                                                                                                                                                                                                                                                                                                                            ----HPL----FIWLKMRISKLVPWMILGSLLYV--SMICVFHSKYAGFMVPYFLRKFFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGGFTTTLYTSLHGYFVFGPTGCNVEGFFATLGGEIALWSLVVLAIERYVVVCKPMSNFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MLAAYM----FLLIVLGFPINFLTLYVTV------QHKKLRTPLNYILLNLAVADLFMV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 21.8
70; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 130.5; DB Pred. No. 0.0012;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128;
                                                       (domestic sheep)
#text_change 07-May-1999
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kinase) #status
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                                            216 RVPGRGAPISALLSILSFLILYFSHCMIKVFLSSLKFHIRRFIFL---
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                                                                                                                                                                                                                                                                                                                                                                                        Local
         QKAEKEVTRMVIIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAKSSSVY--
                                                                            GALYFTLKPEINNE---SFVIYMFVVHFSIPLIVIFFCYGQLVFTVKEAAAQQQES-ATT
                                                                                                  --KFFSQNATIQKEDTLAIQIESFVAEFSVPLLIFFLFAVLLLIFSLGRHTROMRNTVAGS
                                                                                                                                                       FGENHAIMGVAFTWVMALACAAPPLVGW--
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F;114-133/Domain: transmembrane #status predicted <TMM3>
F;135-175/Domain: transmembrane #status predicted <TMM4>
F;135-175/Domain: transmembrane #status predicted <TMM4>
F;203-230/Domain: transmembrane #status predicted <TMM5>
F;255-276/Domain: transmembrane #status predicted <TMM5>
F;265-309/Domain: transmembrane #status predicted <TMM5>
F;265-309/Domain: transmembrane #status predicted <TMM7>
F;276-Modified site: acetylated amino end (Met) #status predicted F;265/Binding site: carbohydrate (Asn) (covalent) #status predicted F;265/Binding site: palmitate (Cys) (covalent) #status predicted F;265/Binding site: palmitate (Cys) (covalent) #status predicted F;332,323/Binding site: phosphate (Thr) (covalent) #status predicted F;334,338,343/Binding site: phosphate (Thr) (covalent) (by rhodopsin kinase)
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A; Accession: A93264; FIND
A; Residues: 240-348 FIND

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Keywords: acetylated amino end; chromoprotein; eye; G
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A;Residues: 1;40-44;45-86;87-111;144-155;156-163;164-183;184-207;208-241 <BRE>
R;Findlay, J.B.C.; Brett, M.; Pappin, D.J.C.
Nature 293, 314-316, 1981
A;Title: Primary structure of C-terminal functional sites in ovine rhodopsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. J. 211, 661-670, 1983
A;Title: Isolation and characterization of the
A;Reference number: A90319; MUID:83282605
A;Accession: A90319
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A; Note: peptides and unsequenced
R; Brett, M.; Findlay, J.B.C.
Biochem. J. 211, 661-670, 1983
                                                                                                                                                                                                                                                                                                                                                              1 MLESHLIIYFLLAVIQFLLGIFTNGIIYVVNGIDLIKHRKM-APLDLLLSCLAVSRIFLQ 59
                                                                                          FGGFTTTLYTSLHGYFVFGPTGCNLEGFFATLGGEIALWSLVVLAIERYVVVCKPMSNFR
                                                                                                                                                                               LFIFYVNVIVIFFIEFIMCSANCAILLFI----NELELW----LATWLGVFYCAKVASVR 111
----HPL----FIW----LKMRISKLVPWMILGSLLYVSMICVFHSKYAGFMVPYFLR---
                                                                                                                                                                                                                                                                                        MLAAYM---FILIVLGEPINELTLYVTV-----QHKKLRTPLNYILLNLAVADLEMV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 129.5; DB Pred. No. 0.0014; 2; Mismatches 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71;
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     157
                                                                                          147
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C; Superfamily: vertebrate rhodopsin
C; Keywords: chromoprotein; eye; G protein-coupled recept
C; Keywords: chromoprotein; eye; G protein-coupled recept
F; 37-61/Domain: transmembrane #status predicted <TM2>
F; 74-96/Domain: transmembrane #status predicted <TM3>
F; 114-133/Domain: transmembrane #status predicted <TM5>
F; 153-175/Domain: transmembrane #status predicted <TM6>
F; 253-276/Domain: transmembrane #status predicted <TM6>
F; 253-276/Domain: transmembrane #status predicted <TM6>
F; 285-399/Domain: transmembrane #status predicted <TM7>
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J. Mol. Biol. 224, 343-358, 1992
A;Title: Localization and DNA sequence of a replication origin A;Reference number: S23398; MUID:92219256
A;Accession: S23398
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A; Residues: 1-348 <GAL>
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S51677
C;Accession: S51677
R;Huber, A.; Baker, B.B.; Sander, P.; Gerdon, G.; Paulsen, R.; Williams, T.P. submitted to the EMBL Data Library, December 1994
A;Bescription: Light-history effects: Levels of rhodopsin, opsin and opsin mR A;Reference number: S51677
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S51677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FGGFTTTLYTSLHGYFVFGPTGCNLEGFFATLGGEIALWSLVVLAIERYVVICKPMSNFR 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTRMVILMVVFFLICWFPYAGVAFYIFTHQGSNFGPIFMTLPAFFAKSSSIY---NPVIY 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----HPL----FIWLKMRISKLVPWMILGSLLYV--SMICVFHSKYAGFMVPYFLRKFFS 161
                                                                                                                                                                                                                                                                                                                                                                                       APISALLSILSFLILYFSHCMIKVFLSSLKFHIRRFIFL----FFILVIGIYPSGHSLIL 277
                                                                                                                                                                                                                                                                                                                                                                                                                                    NESFV-----IYMFVVHFTIPLIVIFFCYGQLVFTVKEAAAQQQES-ATTQKAEKE 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FGENHAIMGVVFTWI-MALACAAP-PLVGWSRYIPEGMQCSCGVDY-----YTLKPEVN
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Pred. No. 0.0017;
3; Mismatches 129;
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10-Sep-1999 #text_change 10-Sep-1999
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                                  opsin mRNA
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A;Molecule type: mRNA
A;Residues: 1-348 4HUB>
A;Residues: 1-348 4HUB>
A;Cross-references: EMBL:Z46957; NID:g603874; PIDN:CAA87081.1; PID:g603875
A;Cross-references: EMBL:Z46957; NID:g603874; PIDN:CAA87081.1; PID:g603875
C;Superfamily: vertebrate rhodopsin
C;Keywords: chromoprotein; eye; G protein-coupled receptor; lipoprotein; pl
C;Keywords: chromoprotein; eye; G protein-coupled receptor; lipoprotein; pl
F;296/Bindding site: retinal (Lys) (covalent) #status predicted
F;322,323/Binding site: palmitate (Cys) (covalent) #status predicted
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C;Date: 15-Oct_1999 #sequence_revision 15-Oct-1999 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein W05B5.2 - Caenorhabditis elegans
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A;Introns: 48/2; 97/3; 146/3; 185/1;
C;Superfamily: neurokinin 1 receptor
                                                                                                                                                                                                                                                                                                                             A; Experimental source: clone C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-382 <WIL>
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                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: EMBL: Z82071; PA; Experimental source: clone W05B5
                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A; Accession: T26188
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Best Local Similarity
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Best Local
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    108
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                                    51 LAVSRIFLQLFIFYVNVIVIFFIEFIMCSANCAILLFINELELWLATWLGVFY-CAKVAS 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QKAEKEVTRMVIIMVIFFLICWLPYASVAMYIFTHQGSNFGPIFMTLPAFFAKTASIY--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----HPL----FIW---LKMRISKLVPWMILGSLLYVSMICVFHSKYAGFMVPYFLR---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - NPIIYIMMNKQF----RNCMLTTLCC
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LAIADLLILLECLPLTVVNDVTKTEWESAVECKSVNEVNNTSVYVSIMSLVEITCERWRA 167
                                                                           VYILASMM--VIGVIGNTLVVVVVATNKSMVGRMGTGNRGNRVVCSMFHKRNALNLVLMN 107
                                                                                                               IYFLLAVIQFLLGIFTNGIIVVV------
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60; Conserv
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                                                                                                                                                                                                                                                                                                                                                                     PIDN:CAB04918.1;
                                                                                                                                                                        Score 125; DB 2;
Pred. No. 0.0035;
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                                                                                                                                                          Mismatches 105;
                                                                                                                                                                                                                                                                        216/3; 268/2;
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                                                                                                                                                                                               Length 382;
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Nucleic A
A; Title:
                                   NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Cyanidioschyzon merolae C;Species: mitochondrion Cyanidioschyzon merolae C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 20-Jun-2000 C;Accession: D58931
R;Ohta, N.; Sato, N.; Kuroiwa, T.
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E22845
E22845
E22846
hypothetical protein 4 - Trypanosoma brucei mitochondrion C; Species: mitochondrion Trypanosoma brucei
C; Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_
C; Accession: E22845
C; Accession: Parakenhoff, J.; De Vries, B.F.; Sloof
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R;Hensgens, L.AM.; Brakenhoff, J.; De Vries, B.F.; Sloof, P.; Tromp, M.C.; Van Boom, J. Nucleic Acids Res. 12, 7327-7344, 1984
A;Title: The sequence of the gene for cytochrome c oxidase subunit I, a frameshift contended in axi-circle DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Superfamily: hypothetic
C; Keywords: mitochondrion
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C; Superfamily: hypothetical
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A; Residues: 1-445 <HEN>
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A;Accession: E22845
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N.; Sato, N.; Kuroiwa, T.
Acids Res. 26, 5190-5198, 1998
...Structure and organization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
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                                                                                                                                                                                                                                                                                                                                                                        ---TLLILFKLYIAFLILFM----EQLYIRLGVFIFI-----YMLTFYILFCF--
                                                                                                                                                                                                                                                                                                                                                                                                  VRHPLFIWLKMRISKLVPWMILGSLLYVSM-ICVFHSKYAGFMVPYFLRKFFSQNATIQK 168
                                                                                                                                                                                                                                                                                                                                                                                                                                    YYMLNLINFILLFILLYFMILNYCFFLCDFCFLVFDEE-----WLGILCLFY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FY----VNVIVIFFIEFIMCSANC-----AILLFINELELWLATWLGV---FYCAKVAS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIIIIIQYIIIFLFIFINHIIIISILFEI-----FSLLLFLLLMSSRFGYKILVLMY 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLLAVIOFL---LGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIF----LQLFI 62
                                                                                                                                                                                                                                         LLEVLSVNNFCFLFLIFISTKNYIFYLYLNFHLIYSISLVLLIII------YYFFIIYNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RVPGRGAPISALLSILSFLILYFSHCMIKVFLSSLKFHI 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRCKESWSEEFQKNYQLLQTIFSFY----LPLLVISILCLHMVRTL--HFSANYLTVANR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITYPLKSPFVRTR-----SVIGGIWFIAMFLSSPEPVTLHLAGAPFVRPNPTTKWG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 124.5; DB Pred. No. 0.0044;
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   the mitochondrial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94;
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the unicellular
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A;Reference number: A58930; MUID
A;Accession: D58931
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-500 <ARN>
A;Cross-references: GB:D89861; N
C;Genetics:
A;Gene: nad2
R; Inglehearn, C.F.; Bashir, R
Am. J. Hum. Genet. 48, 26-30,
A; Title: A 3-bp deletion in the
A; Reference number: A36537; M
A; Accession: A36537
                                                                                            hattacharya, S.; Humphries, P.
Am. J. Hum. Genet. 47, 941-945, 1990
A;Tille: Autosomal dominant retinitis pigmentosa:
A;Reference number: A36235; MUID:91051574
A;Accession: A36235
A;Molecule type: DNA
A;Residues: 18-27 <FAR>
A;Residues: 18-27 <FAR>
                                                                                                                                                                                                                                                                                                        R: Nathans, J.; Hogness, D.S.
Proc. Natl. Acad. Sci. U.S.A. 81, 4851-4855, 1984
A;Title: Isolation and nucleotide sequence of the
A;Reference number: A41200; MUID:84272729
A;Accession: A41200
                                                                                                                                                                                                                                                                                                                                                                                                  C:Species: Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
C:Accession: A41200; A36535; A36537; I51864; I64813; I64814
                                                                                                                                                                                                                                A;Cross-references: GB:K02281; NID:g1236136; PIDN:AAC31763 1; R;Farrar, G.J.; Kenna, P.; Redmond, R.; McWilliam, P.; Bradle;
                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-348 <NAT>
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C:Superfamily: NADH dehydrogenase (ubiquinone) chain 2
C:Keywords: membrane-associated complex; mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 LESHLIIYFLLAVIQ------FLLGIFTNGIIV------VVNGIDL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKLVPWMILGSLLYVS--MICVFHSKYAGF-----MVPYF-----LRKFFSQ 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VNVIVIFFIEFIMCSANCAILLFINELELWLATWLGVFYCAKVASVRHPLFI--WLKMRI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P----PIAGFFTKLIVFLTCLKSSLYSLVIFAITISCLATFYYIRIIKIIYFDNCNVWLI
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19.8%;
                the rhodopsin MUID:91090106
                                                        R.; Lester, D.H.;
0, 1991
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                                                                       A.C.;
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                                                                                                                                                                                                                                PID:g1236137
y, D.G.; Hump
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                               autosomal dominant re
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                                                                                                                                                                                                                                                                                                                                                    human rhodopsin.
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                                                                                                                                                                   rhodopsin proline->h
                                                                     Bhattacharya,
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R;Sheffield, V.C.; Fishman, G.A.; Beck, J.S.; Kimura, A.E.; Stone, E.M. Am. J. Hum. Genet. 49, 699-706, 1991
A;Title: Identification of novel rhodopsin mutations associated with retinitis pigmentos
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A; Residues: 248
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A;Map position: 3q21.3-3q24
A;Introns: 121/1; 177/2; 232/3; 312/3
A;Note: defects in this gene can result in retinitis pigmentosa C;Superfamily: vertebrate rhodopsin
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A;Residues: 264-266,'L',268-270 <SH3>
A;Cross-references: GB:S55874; NID:g235662; PIDN:AAB19832.1;
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A; Residues: 14-16, 'M', 18-20 <SI
A; Cross-references: GB:S55797;
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A; Accession: I51864
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A;Status: translated from GB/EMBL/DDBJ
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A;Residues: 179-181,'S',183-185 <SH2>
A;Cross-references: GB:S55799; NID:g235660; PIDN:AAB19831.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;277-284,/Domain: extracellular *status predicted <EX4>;285-309/Domain: transmembrane *status predicted <TM7>;310-348//Domain: intracellular *status predicted <TM7>;310-348//Domain: intracellular *status predicted <IN4>;1/Modified site: acetylated amino end (Met) *status predicted ;2,15/Binding site: carbohydrate (Asn) (covalent) *status predicted ;210-187/Disulfide bonds: *status predicted ;210-187/Disulfide bonds: *status predicted ;296/Binding site: retinal (Lys) (covalent) *status predicted ;322,323/Binding site: palmitate (Cys) (covalent) *status predicted ;322,323/Binding site: phosphate (Ser) (covalent) (by rhodopsin ;334,338,343/Binding site: phosphate (Thr) (covalent) (by rhodopsin kinase)
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Best Local Similarity
Matches 68; Conserv
                 188 GIDYYTLKPEVNNE---SFVIYMFVVHFTIPMIIIFFCYGQLVFTVKEAAAQQQES-ATT
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                                                                                                                                --KFFSQNATIQKEDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGS 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGGFTSTLYTSLHGYFVFGPTGCNLEGFFATLGGEIALWSLVVLAIERYVVVCKPMSNFR 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----HPL----FIW---LKMRISKLVPWMILGSLLYVSMICVFHSKYAGFMVPYFLR---
                                                                                                                                                                                                                                                          FGENHAIMGVAFTWVMALACAAPPLAGW:
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                                                          243
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pheromone receptor VN4 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Or-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 29-Sep-1999
C;Accession: 161746
R;Dulac, C.; Axel, R.
Cell 83, 195-206, 1995
Cell 83, 195-206, 1995
A;Reference number: A57223; MUID:96028094
A;Reference number: A57223; MUID:96028094
A;Accession: 161746
A;Rotession: 161746
A;Rotession: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-335 <RES>
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                                                                                                                                                                                         G protein-coupled receptor 41 - human
C;Species: Homo sapiens (man)
C;Date: 03-Dec-1997 #sequence_revision 03-Dec-1997
C;Accession: JC5715
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                                                                     R;Sawzdargo, M.; George, S.R.; Nguyen, T.; Xu, Biochem. Biophys. Res. Commun. 239, 543-547, 15 A;Title: A cluster of four novel human G protei A;Reference number: JC5714; MUID:98008875 A;Accession: JC5715 A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                       В
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                                     A; Molecule type: mRNA
A; Residues: 1-346 <SAW>
A;Cross-references: GB:AF024688; NID:g2612947; PIDN:AAB86711.1; PID:g2612948 C;Superfamily: G protein-coupled receptor 43
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63; Conser
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                                                                                                                                                                ı, S.; Kolakowski Jr., L.F.; O'Dowd,
1997
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A;Reference number: Z20332

A;Accession: T27253
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-547 <WIL>
A;Cross-references: EMBL:AL021501; PIDN:CAA16414.1; GSPDB:GN00023; CESP:Y61B8A.1
A;Experimental source: clone Y61B8A
C;Genetics:
A;Genetics:
A;Gene: CESP:Y61B8A.1
A;Map position: 5
A;Introns: 121/1; 197/2; 330/1
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Matches
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                                                                                                                                94 WL-----ATWLGVFYCAKVASVRHPLFIWLKMRISKLVPWMILGSLLYVS-MICVFHSK 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 VAGILAATILNELVCEGPYNVSHVVGYICGESPAWRIYVTLLSTLNSCVDDEVYYE 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 224 ISALL -- SILSFLILY ---- FSH ----- C----- MIKVELSSLKFHIRRFIFLF 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 TLAI----QIFSFVAEFSVPLLIFLFAVLLLIFSLGR---HTROMRNTVAGSRVPGRGAP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 QAGLVSVACWLLASAHCSVVYVIEFSGDISHSQ------GTNGTCYLEFRKD 176
                                                                                                                                                                                                                                     35
                                                                                                                                                                                                                                                                         / Match 8.1%; Score 122.5; DB 2; Local Similarity 24.1%; Pred. No. 0.0077; No. 66; Conservative 38; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
LIPEDQDAARQFALTLHPCPTREFFTSEVLIILADNILIERFIWIFPIFGVYFASFPLFQ
                                                                                                                                                                          LINHLECALLDLLLCIFSTVYYELPMYGVEFYGVFSWFGIPNVL----QILL-----V 324
                                                                                                                                                                                                              LIKHRKMAPLDLLLSCLAVSRIFLQLE-IFYVNVIVIFFIEFIMCSANCAILLFINELEL
                                                                                                 WLMMMLTGASYVYFFKC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QLAILLPVRLEMAVVLFVVPLIITSYCYSRLVWILGRGGSHRRQRR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---ISKLVPWMILG----SLLYVSMIC---VFHSKYAGFMVPYFLRKFFSQNATIQ----KED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANGMHWPLPFILCPLSG--FIFFTTIYL-TALFLAAVSIERFLSVAHPL--WYKTRPRLG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I----FFIEFIMCSANCAILLFINELELWLATWLGVFYCAKVASVRHPLFIMLKMR---- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                        -----YAGEMVPYFLRKFFSQNATIQKEDTLAIQIFSEVAE-FSVPLLIF-LFA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.1%;
24.0%;
                                                                                       --RSSILVQNKFRITRQKTRMIYYSLFFIPWMLTTYFEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 122.5; DB 2; Length 346;
Pred. No. 0.0052;
3; Mismatches 93; Indels 79
                                                                                                                                                                                                                                                                         83;
                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                    547;
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                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                          93
                                                                                       378
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C;Keywords: chromoprotein; eye; G protein-coupled receptor; glycoprotein; lipoprotein C;Keywords: chromoprotein; eye; G protein-coupled receptor; glycoprotein; lipoprotein F;37-61/Domain: transmembrane #status predicted <TMM2>F;14-96/Domain: transmembrane #status predicted <TMM3>F;113-175/Domain: transmembrane #status predicted <TMM3>F;203-230/Domain: transmembrane #status predicted <TMM5>F;203-230/Domain: transmembrane #status predicted <TM6>F;203-276/Domain: transmembrane #status predicted <TM6>F;203-276/Domain: transmembrane #status predicted <TM7>F;285-309/Domain: transmembrane #status predicted <TM7-F;285-309/Domain: transmembrane #status predicted <TM7-F;285-309/Domain: transmembrane #status predicted <TM7-F;285-309/Domain: transmembrane #status predicted <TM7-F;285-309/Domain: transmembrane #status predicted <TM7-F;38
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C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A23665; S01656
R;Al-Ubaidi, M.R.; Pittler, S.J.; Champagne, M.S.; Triantafyllos, J.T.; McGinnis, J.F.
J. Biol. Chem. 265, 20563-20569, 1990
A;Title: Mouse opsin. Gene structure and molecular basis of multiple transcripts.
A;Reference number: A23665; MUID:91056108
A;Accession: A23665
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A:Reference number: S01656; MUID:89005694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Introns: 121/1; 177/2; 232/3;
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A; Residues: 1-348 <BAE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: S01656
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A; Residues: 1-348 <ALA>
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278 ILGNPKLKQNAKKFLLHSKCC 298
                                                                                                                                                                     222
                                                                                                                                                                                                                            200 NESFV------IXMEVVHETIPMIVIFFCYGQLVETVKEAAAQQQES-ATTQKAEKE
                                                                                                                                                                                                                                                                                                                                                                                         148 FGENHAIMGVVFTWI-MALACAAP-PLVGWSRYIPEGMQCSCGIDY-----YTLKPEVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 ----HPL----FIWLKMRISKLVPWMILGSLLYV--SMICVFHSKYAGFMVPYFLRKFFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MLESHLIIYELLAVIQELLGIETNGIIVVVNGIDLIKHRKM-APLDLLLSCLAVSRIFLQ 59
                                                                                                                                            APISALLSILSFLILYFSHCMIKVFLSSLKFHIRRFIFL----FFILVIGIYPSGHSLIL 277
                                                                                                                                                                                                                                                                                                             QNATIQKEDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGSRVPGRG
                                                                   VTRMVIIMVIFFLICWLPYASVAFYIFTHQGSNEGPIFMTLPAFFAKSSSIY---NPVIY 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LFIFYVNVIVIFFIEFIMCSANCAILLFI----NELELW----LATWLGVFYCAKVASVR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MLAAYM---FULIVLGFPINFLTLYYTV-----QHKKLRTPLNYILLNLAVADLFMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FGGFTTTLYTSLHGYFVFGPTGCNLEGFFATLGGEIALWSLVVLAIERYVVVCKPMSNFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               312/3
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307

IM----LNKQFRNCMLTTLCC

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J. Mol. Evol. 40, 594-600, 1995
A;Title: Paralogous origin of the rhodopsinlike opsin genes in lizards.
A;Reference number: I51319; MUID:95371134
A;Accession: I51319
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-355 <KANP
A;Cross-references: GB:S79167; NID:g1042072; PIDN:AAB35062.1; PID:g1042073
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Anolis carolinensis (green anole)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Aug-1999
C;Accession: I51319
R;Kawamura, S:; Yokoyama, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: rh2Ac
A;Introns: 121/1; 177/2; 232/3; 312/3
A;Introns: 121/1; 177/2; 232/3; 312/3
C;Superfamily: vertebrate rhodopsin
C;Keywords: chromoprotein; eye; G protein-coupled receptor; lipoprotein; phosphoprotein
C;Keywords: chromoprotein; eye; G protein-coupled receptor; lipoprotein; phosphoprotein
F;296/Binding site: retinal (Lys) (covalent) #status predicted
F;322,323/Binding site: palmitate (Cys) (covalent) #status predicted
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A;Cross-references: GB:AE001179; GB:AE000783; NID:g2688738; PIDN:AAC67146.1; PID:g26887.
A;Experimental source: strain B31
C;Superfamily: mviN protein
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-512/Product: virulence factor mviN protein homolog #status predicted <MAT>
                                                                                                         A; Molecule type: DNA
A; Residues: 1-512 <KLE>
                                                                                                                                              A; Status: preliminary; nucleic acid sequence not shown; translation
                                                                                                                                                                 A; Reference number: A70100; MUID:98065943
A; Accession: A70201
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Best Local Similarity 23.6%;
Matches 62; Conservative 4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGISFTWF-MSFSCAAP-PLLGWSRYIPEGMQCSCGPDY---
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Best Local
                                                                                                                                                                                                                                                                      136 YLVLYILLISLSSI-----FVSVLNSYKIFFIPSFSPIMLSFG-----IILSIFLFY 182
                                                                                                                                     228
                                                                                                                                                                                                     183 GRFGIYSAVIGVIFGGFLOFLIPFANCLMIGF-----AWKPTFY-----FREKVF
                                                                    281
 320
                                                                                                                                                                                                                                                                                                      5 HLIIYELLAVIQELLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFIQLEIFY 64
                                VAGSRVPGRGAPISALLSILSFLILYFSHCMIKVFLSSLKFHI 254
                                                                    YISIATV-----
                                                                                                 FSQNATIQKEDTLAIQIFSFVAEFSV-----PLLIFLFAVLLLIFSLGRHTROMRNT 211
                                                                                                                                   LNFLTRWLRMIFGFSISIITQQIS-----FALASTLEIGSVSILSNAVVYYQLPVGI--F
                                                                                                                                                                 I-----WIKM------RISKLVPWMIIGSLLYVSMICVFHSKYAGFMVPYFLRKF 159
                                                                                                                                                                                                                                    -----VNVIVIFFIEFIMCSANCAILLFINELELMLATMLGVFYCAKVASVRHPLF 115
   ----IP----
                                                                                                                                                                                                                                                                                                                                            60;
                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                            8.0%; Score 121; DB 1; Length 512; 21.2%; Pred. No. 0.0097;
----VSFLMFIWSDYILNLFLMGGKFSI 345
                                                                    IFPKMAEHAVLGNNIKLNALLVDGIKILLLIF---
                                                                                                                                                                                                                                                                                                                                                43;
                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                   74;
                                                                                                                                                                                                                                                                                                                                                   Indels 106;
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Search completed: March 15, Job time: 467 sec 2001, 13:00:06

98.50 98

98.50 159.

165.36 0

5.36 0.1170 0.1647 2

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/cgn2_6/ptcodata/2/ina/5_COMB.seq:US-08-770-339-20+ 120.50 175.04 0.0338 /cgn2_6/ptcodata/2/ina/5E_COMB.seq:US-08-466-855A-1 106.00 160.94 0.2038 929-6/ptcodata/2/ina/5E_COMB.seq:US-08-006-644-93 106.00 160.15 0.285 955-666-644-93-106.00 160.15 0.285 955-666-644-93-106.00 160.15 0.285 955-6972_6/ptcodata/2/ina/5E_COMB.seq:US-08-006-644-93-106.00 160.15 0.285 955-6972_6/ptcodata/2/ina/5E_COMB.seq:US-08-470-77-7 104.50 175.59 0.0315 1958-6072_6/ptcodata/2/ina/5E_COMB.seq:US-08-470-77-7 104.50 175.59 0.0315 1958-6072_6/ptcodata/2/ina/5E_COMB.seq:US-08-470-77-7 104.50 175.59 0.0315 1958-6072_6/ptcodata/2/ina/5E_COMB.seq:US-08-470-77-7 104.50 175.59 0.0315 1958-6072_6/ptcodata/2/ina/5E_COMB.seq:US-08-470-7017-7 104.50 175.59 0.0315 1958-6072_6/ptcodata/2/ina/5E_COMB.seq:US-08-470-7017-7 104.50 175.59 0.0315 1958-6072_6/ptcodata/2/ina/5E_COMB.seq:US-08-470-917-7 104.50 175.59 0.0315 1958-6072_6/ptcodata/2/ina/5E_COMB.seq:US-08-470-919-103.00 173.11 0.0433 185-6072_6/ptcodata/2/ina/5E_COMB.seq:US-08-153-848-39 + 103.00 173.11 0.0433 185-6072_6/ptcodata/2/ina/5E_COMB.seq:US-08-607-809-3 + 102.50 178.51 0.0217 1080-290-290-2-6/ptcodata/2/ina/5E_COMB.seq:US-08-590-33+ 102.50 178.51 0.0217 1080-290-2-6/ptcodata/2/ina/5E_COMB.seq:US-08-590-33+ 102.50 178.51 0.0217 1080-290-2-6/ptcodata/2/ina/5E_COMB.seq:US-08-591-378-3 102.50 178.51 0.0217 1080-290-2-6/ptcodata/2/ina/5E_COMB.seq:US-08-801-094-13 100.00 178.51 0.0217 1080-2-6/ptcodata/2/ina/5E_COMB.seq:US-08-801-094-13 100.00 178.51 0.0217 1080-2-6/ptcodata/2/ina/5E_COMB.seq:US-08-801-094-13 100.00 178.99 0.0204 674-691-6-6/ptcodata/2/ina/5E_COMB.seq:US-08-801-094-13 100.00 178.99 0.0204 674-691-6-6/ptcodata/2/ina/5E_COMB.seq:US-08-801-094-13 100.00 178.99 0.0204 674-691-6-6/ptcodata/2/ina/5E_COMB.seq:US-08-801-094-13 100.00 178.99 0.0204 674-691-6-6/ptcodata/2/ina/5E_COMB.seq:US-08-91-094-13 100.00 179.99 0.0204 674-691-6-6/ptcodata/2/ina/5E_COMB.seq:US-08-91-094-13 100.00 179.99 0.0204 674-691-6-6/ptcodata/2/ina/5E_COMB.seq:US-08-08-20-056-6 99.00 160.69 0.2129 277-691-6/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database: Issued_Patents_NA:*
Database sequences: 280836
Database length: 80580151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search information blo
Query: US-09-510-332-1
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-QC/GP12_1/USPF0_spool/US99510332/runat_06032001_093637_13647/app_query.fasta_1.359
-QC/GP12_1/USPF0_spool/US99510332/runat_06032001_093637_13647/app_query.fasta_1.359
-QCAPCP14_000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QCAPCP14_000 -QGAPEXT=0.000 -XGAPCP=10.000 -XGAPCXT=0.500
-FGAPCP=4.500 -QGAPEXT=7.000 -XGAPCP=10.000 -YGAPCXT=0.500
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-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
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-NORM=ext -MINLEN=0 -MAXLEN=200000000
-USER=US09510332_@CGN1_1_54 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cgn2_6/ptodata/2/ina/6_COMB.seq:US-08-931-999-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-805-123C-1 + 
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-033-081B-1 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-820-521-1 + /cgn2_6/ptodata/2/ina/5_COMB.seq:US-08-728-603-16 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length: 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -THREADS-1
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122.50 212.37 0.0003
120.50 213.32 0.0002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-805-123C-1
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                                                                                                                                                                                                                                      alignment_block:
US-09-510-332-1 x US-07-805-123C-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/07805123C Patent No. 5262529
                                                                                                                                                                                                 Align seg 1/1 to: US-07-805-123C-1 from: 1
                                                                                                                                                                                                                                                                                            Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Dryja, Thaddeus
APPLICANT: Berson, Eliot L.
TITLE OF INVENTION: DIAGNOS
TITLE OF INVENTION: DEGENER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PS/2 Model 50Z or 55S;
OPERATING SYSTEM: MS-DOS (Version 5
SOFTWARE: Wodderfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/469,215
FILING DATE: January 24, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                         450 CCCCATCAACTTCCTCACGCTCTACGTCACCGTC
34 spLeuIleLysHisArgLysMet...AlaProLeuAspLeuLeuLeuSer 49 :::||||::: :::||||
                                                                                       17 eLeuLeuGlyIlePheThrAsnGlyIleIleValValValAsnGlyIleA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 00:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US
FILING DATE: 19911211
                                                                                                                                                            1 MetLeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIleGlnPh
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TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02110-2804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (617) 542-8906
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                                                                                                                                                                                                                                                                                            Length: 328
Gaps: 16
t Identity: 20.732
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seq\_documentation\_block: seq\_name: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:US-08-033-081B-1 1234 .CGGAACTGCATGCTCACCATCTGCTGCCGC 1266 1198 ...AACCCTGTCATCTATATCATGATGAACAAGCAGTTC..... 1233

Phe 143	127 roTrpMetIleLeuGlySerLeuLeuTyrValSerMetIleCysValPhe     :::       :::   :::::   :::::
726	728
1P 127	110 largHisProLeuPheIleTrpLeuLysMetArgIleSerLysLeuVal
	78 TIPLEGRADIAL TERRORS TO TERROR
11	• o
eu 93 :: TT 759	79 erAlaAsnCysAlaIleLeuLeuPheIleAsnGluLeuGluLeu ;;;;;   ;;;    ;;;
SS 79	62 ePheTyrvalAsnvalIlevalIlePhePheIleGluPheIleMetCysS
Il 62 :: TT 859	48 LeuSerCysLeuAlaValSerArgIlePheLeuGlnLeuPheIl 
to: 6755	Align seg 1/1 to reverse of: US-08-931-999-4 from: 1
	alignment_block: US-09-510-332-1 x US-08-931-999-4/rev
	50.840 Percent Identity: 26.47
	124.50 Length: 2
	30 - SI
	ANTI-SENSE: NO ORIGINAL SOURCE
•	MOLECULE TYPI HYPOTHETICAL
	TOPOLOGY: unknown
	TYPE: nucleic acid
	; INFORMATION FOR SEQ ID NO: 4: ; SEQUENCE CHARACTERISTICS: ; SEQUENCE CASE: PAGE SAIS:
	TELECOMMUNICATION INFORMATION:
	~
	CLASSIFICATION:
	CURRENT APPLICATION DATA:
	OPERATING SYSTEM: PC-DOS/MS-DOS
	opy disk
	ZIP: 64108
	STATE:
	STREET: 2405 Grand Boulevard, Suite
	: illiams, Timmons

```
APPLICANT: Bergsma, Derk
APPLICANT: Ganesh, Sathe
APPLICANT: Fuetterer, Wendy
APPLICANT: Mao, Joyce
ITITLE OF INVENTION: CDNA CLONE HNFDY20 THAT ENCODES
INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTPY: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-820-521-1
                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,521
FILING DATE: 19-MAR-1997
CTACCTETCATTON: 475
                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 lPheLeuSerSerLeuLysPheHisIleArgArgPhe...IlePheLeup 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 hrileGlnLysGluAspThrLeuAlaIleGlnIlePheSerPheValAla 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360 CTTTCTG...CGGCTTGCGTTTCGCGTCGCTTTTTTTTTCGCTGGTTTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 lySerArgValProGlyArgClyAlaProIle.....SerAlaLeuLeu 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      586 CTGTG.....GTTGGCTTTTGCTTTTTTTTTTTTCTGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 725 ..TGGGCCGTTTTG...TCCGTTTTGTTTGCTTCGTTTTTCTTGCGCTTT 681
REGISTRATION NUMBER: 34,344
                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 19406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hePheIleLeuVal 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTCTTCTGTGTGTCTTCTTTTTTTTTTTTTTCT.....TTGCGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ePheSerLeuGlyArgHisThrArgGlnMetArgAsnThrVal...AlaG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....................LeuArgLysPhePheSerGlnAsnAlaT 165
                     Han, William T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        552
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alignment_block:
us-09-510-332-1 x us-08-820-521-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-820-521-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: US-08-820-521-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1841 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                      160 eSerGlnAsnAlaThrIleGln.....LysGluAspThrLeuAlaI 174
                                                                                                                                                                                                     144 HisSerLysTyrAlaGlyPheMetValProTyrPheLeuArgLysPhePh 160
                                                                                                                                                                                                                                                 720 CTGCTCACTGCAGCGTGGTCTACGTCATAGAATTCTCAGGGGACATCTCC
                                                                                                                                                                                                                                                                                                  132
                                                                                                                                                                                                                                                                                                                                626 CGCTTCCTGAGTGTGGCCCACCCCCTG....TGGTACAAGACCCGGCC 669
                                                                                                                                                                                                                                                                                                                                                                                                                                          106 LysValAlaSerValArgHisProLeuPheIleTrpLeuLysMetArg.. 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                535 CCTGCCCTTCATCCTCTGCCCCACTCTCTGGA.....TTCATCTTCTTCA 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    388 GCTGGCCCTGGTGGTCTTCGTGGGCAAGCTGCAGCGCCGCCCGGTGGCC. 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     341 TTCTCGGTGTACCTTCTCACTTTCCTGGTGGGGCTCCCCCTCAAC...CT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: GITELECOMMUNICATION INFORMATION.
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 LeuPheIlePheTyrValAsnValIleValIle.....phePh 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 roLeuAspLeuLeuSerCysLeuAlaValSerArgIlePheLeuGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 eIleValValAsnGlyIleAspLeuIleLysHisArgLysMetAlaP 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 PheLeuLeuAlaValIleGlnPheLeuLeuGlyIlePheThrAsnGlyIl 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 610-270-4026
TCCTCCTGCCGTGCGGCTGGAGATGGCTGTGGTCCTCTTTGTGGTCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCACCATCTATCTC...ACCGCCCTCTTCCTGGCAGCTGTGAGCATTGAA 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGTTCCTGCCTTTCCGCATGGTGGAGGCAGCCAATGGCATGCACTGGCC
                                       le......GlnIlePheSerPheValAlaGluPheSerValPro 186
                                                                                                                                                                                                                                                                                    ly......SerLeuLeuTyrValSerMetIleCys.....ValPhe 143
                                                                                                                                                                                                                                                                                                                                                                        snGluLeuGluLeuTrpLeuAlaThrTrpLeuGlyValPheTyrCysAla 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eIleGluPheIleMetCysSerAlaAsnCysAlaIleLeuLeuPheIleA 89
                                                                               GCCACCAATGGGACCTGCTACCTGGAGTTCCGGAAGGACCAGCTAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..GTGGACGTGCTCCTGCTCAACCTGACCGCCTCGGACCTGCTGCTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122.50
0.833
49.662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GH50011
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Ö
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18
23.986
                                                                                                                                                                                                                                                   769
                                                                                                                                                                                                                                                                                                                                  719
                                                                               827
                                                                                                                                                                  778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59
```

														-					
<pre>seq_documentation_block: ; Sequence 20, Application US/08770379</pre>	<pre>seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-770-379-20</pre>	244 LysValPheLeuSerSerLeuLysPheHisIleArgArg 256     :::     845 TACCACGTACTAAATCTACTGGACACTCTGCTAAGGCGA 883	227 euLeuSerlleLeuSerPheLeuIleLeuTyrPheSerHisCysMetIle 243    ::::: ::::  :::	210 nThrValAlaGlySerArgValProGlyArgGlyAlaProIleSerAlaL 227 :	199 PheSerLeuGly	182 luPheSerValProLeuLeuIlePheLeuPheAlaValLeuLeuLeuIle 198     :::       702 GTTTCCTGTTACCCCTGGCCCTCCTTATTCTGTTT 736	166 eGlnLysGluAspThrLeuAlaIleGlnIlePheSerPheValAlaG 182 :::         :::::         :::!!  652 CATGACTGCAGACTGGCGACTGCATGTCAGTTACTGCAG 701	150 PheMetValProTyrPheLeuArgLysPhePheSerGlnAsnAlaThrIl 166	138 erMetlle	121 glieSerLysLeuValProTrpMetIleLeuGlySerLeuLeuTyrValS 138 ::::::::::::::::::::::::::::::::::::	110 ValargHisProLeuPheIleTrpLeuLysMetAr 121	93 euTrpLeuAlaThrTrpLeuGlyValPheTyrCysAlaLysValAlaSer 109 :::    :::::    :::    420 ACTATTTATATGTCTACTTGGATATCTTCAGTGTTGTGTGCGTCAGTCTA 469	76 eMetCysSerAlaAsnCysAlaIleLeuLeuPheIleAsnGluLeuGluL 93  :::	60 LeuphellepheTyrValAsnVallleValllePhePhelleGluPhell 76 :::	43 roleuAspLeuLeuLeuSerCysLeuAlaValSerArgIlePheLeuGln 59 :::   :::	27 eValValAsnGlyIleAspLeuIleLysHisArgLysMetAlaP 43 ::::	11 LeuLeuAlaValIleGlnPheLeuLeuGlyIlePheThrAsnGlyIleI1 27 :::   :::::           :::::	Align seg 1/1 to: US-08-728-603-16 from: 1 to: 1202	alignment_block: US-09-510-332-1 x US-08-728-603-16

```
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,379
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52342
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-770-379-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-510-332-1 x US-08-770-379-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: US-08-770-379-20 from: 1 to: 32207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
Percent Similarity:
24362 ATATCTCTA.....TTGGCAGAAGTGTTGATGTTTTTGTTTCCCAATAT 24405
                                                                                                                                                                      43 roLeuAspLeuLeuLeuSerCysLeuAlaValSerArgIlePheLeuGln 59
:::|||:::||||||
24312 CGATAGATATACTGCTCCTGGGTATCTGCCTAAACTCGCTGTGTCTTAGC 24361
                                                                                                                                                                                                                                                                                                                                              24274 CACCTACATT.....TTTTGCAAGCACCGATCGCGGGCAGGAG 24311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: MOORE, PALTICK S.
APPLICANT: MOORE, PALTICK S.
TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
NUMBER OF SEQUENCES: 20
                                                    76
                                                                                                                          60 LeuPheIlePheTyrValAsnValIleValIlePhePheIleGluPheIl 76
                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                           eMetCysSerAlaAsnCysAlaIleLeuLeuPheIleAsnGluLeuGluL 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120.50
0.867
52.852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 263
Gaps: 14
Percent Identity: 22.433
```

	3	
	CLASSIFICATION: 435	
	APPLICATION NUMBER	
	; SOFTWARE: FastSEQ for Windows Version 2.0 ; CURRENT APPLICATION DATA;	
	COMPUTER: IBM Com- OPERATING SYSTEM:	
	MEDIUM TYP	
	ZIP: 02110-2804	
	CITY: Boston	•
	ADDRESSEE: Fish &	
	NUMBER OF SEQUENCES: 29 CORRESPONDENCE ADDRESS:	
	TITLE OF INVENTION:	
	APPLICANT: Ebisawa, Takashi m. TITLE OF INVENTION: UTCH APPLICATION	
	GENERAL INFORMATION:	
	<pre>seq_documentation_block:     Sequence 1, Application US/08466103A</pre>	
	seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-466-103A-1	
	24869 TACCACGTACTAAATCTACTGGACACTCTGCTAAGGCGA 24907	
	244 LysValPheLeuSerSerLeuLysPheHisIleAr	
24868		
243	N	
24823	11	
227	210 nThrValAlaGlySerArgValProGlyArgGlyAlaProIleSerAlaL :	
24810	ccreerererer	
210	199 PheSerLeuGlyArgHisThrArqGlnMetArqAs	
198 24760	182 luPheSerValProLeuIlePheLeuPheAlaValLeuLeuIle	
24725	24676 CATGACTGCAGACTGCGACTGCATGTCAGAACCGTGTCAGTTACTGCAG	
182	166 eGlnLysGluAspThrLeuAlaIleGlnIlePheSerPheValAlaG	
24675	24635CCGGTCAGCAAGCAGGCCATGTGTTATGAGAACGCCGGGAAA	
166	150 PheMetValProTyrPheLeuArgLysPhePheSerGlnAsnAlaThrIl	
24634	17:	
149	rMetile.	
24584	CCCTCGGATO	
138	121 gIleSerLysLeuValProTrpMetIleLeuGlySerLeuLeuTyrValS	
4	 	
21	TrpLeuLysMetA	
24493	24444 ACTATTTATATGTCTACTTGGATATCTTCAGTGTGTGTGT	
109	93 euTrpLeuAlaThrTrpLeuGlyValPheTvrCvsAlaLvsValAlaSer	

```
NAME/KEY: Coding Sequence;
LOCATION: 32...1291
OTHER INFORMATION:
US-08-466-103A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-510-332-1 x US-08-466-103A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 07-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/261,857
FILING DATE: 17-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00788
TELECOMMUNICATION INFORMATION:
TELEFAX: 617/542-8906
INFORMATION FOR SED ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: US-08-466-103A-1 from: 1 to: 1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 CCTGGGC.....TGTCTG 200
                                                                                                                                                                                                                                               101 ValPheTyrCysAlaLysValAlaSerValArgHisProLeuPheIleTr 117
                                                                                                                                                                                                                                                                                          351
                                                                                                                                                                                                                                                                                                                                                                   201 TCCTGAGGAACAAGAAGCTGCAGAATGCTGGAAATCTCTTTGTTGTCAGT 250
                                                                                                                                436 CCACAGCCTGAGATATGACAAGCTTTATAATCAAAGAAGCACCTGGTGCT 485
                                                                                                                                                       117 pLeuLysMetArgIleSerLysLeuVal.......ProTrpMetI 130 ::::::|| :::||| |||
                                                                                                                                                                                                          386 TCAGTCTTCAACATAACAGCCATAGCTATCAACAGGTATTGCTACATCTG 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 uLeuGlyIlePheThrAsnGlyIleIleValValValAsnGlyIleAspL 35
                                                       486 ACCTTGGCCTGACATGGATACTAACTATAATTGCAATCGTGCCAAACTTT 535
                                                                                         130 leLeuGlySerLeuLeuTyrValSerMetIleCysValPheHisSerLys 146
                                                                                                                                                                                                                                                                                                                                                                                                      67 lileValIlePhePheIleGluPheIleMetCysSerAlaAsnCysAlaI 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 LeuAlaValSerArgIlePheLeuGlnLeuPheIlePheTyrValAsnVa 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 eulleLysHisArgLysMetAlaProLeu...AspLeuLeuLeuSerCys 50
                  147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 LeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIleGlnPheLe 18
                                                                                                                                                                                                                                                                                     TCAGTGGCTTCCTGATGGGACTCAGCGTT.....ATTGGA 385
                                                                                                                                                                                                                                                                                                              leLeuLeuPheIleAsnGluLeuGluLeuTrpLeuAlaThrTrpLeuGly 100
TyrAlaGlyPheMetVal.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118.00
0.752
53.401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08/261,857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       00786/250002
              .ProTyrPheLeuArgLysPhePheSe 161
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; INFORMATION FOR SEVE ID NO. 1. ; SEQUENCE CHARACTERISTICS: ; LENGTH: 8920 base pairs ; TYPE: nucleic acid
NICATION INFORMATION NE: 703-816-4000 : 703-816-4100
STRATION NUMBER: 29. RENCE/DOCKET NUMBER:
FICATION: 433 /AGENT INFORMATI
CATION NUMBER:
RE: PatentIn Release #1.24 APPLICATION DATA:
ER: IBM PC compat
PUTER READABLE FORM: EDIUM TYPE: Floppy o
COUNTR ZIP:
TREET: LIUO NO. JOHANNA GALLE ALLE ALLE ALLE ALLE ALLE ALLE AL
ADDRESSEE: Nixon &
NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
TITLE OF INVENTION: phosphate s
APPLICANT: Flores, Maria V
GENERAL INFORM APPLICANT:
DCUM
seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-446-855A-1
927 TATATGGTGTGAAATCAAAACTTCCGCAAG 958
LyspheHisIleArgA
229 rIleLeuSerPheLeuIleLeuTyrPheSerHisCysMetIleLysValP 246 ::::      :::::       :::
217 ValProGlyArgGlyAlaProIleSerAlaLeuLeuSe 229
777 TTGTACTTTTGCAGTTTGCTGGGCCCCCTTAAACTTTATCGGCCTTGCT 826
214GlySerArg 216
AAAGTTGACACAAACAGACTTGAG
tArgAsnThrValAl
195 LeuLeuLeullePheSerLeuGLyArgH1STDAFGGLI
AGTGTTGTGACATTCTGTTACTTAAGAATA 6
.78 erPheValAlaGluPheSerValProLeuLeuIlePheLeuPheAlaVal l
161 rGlnAsnAlaThrIleGlnLysGluAspThrLeuAlaIleGlnIlePheS 178
GCACATTTGC 58

: sing inear genom
ty: 43.429 Percent Iden x US-08-446-855A-1/rev
e of: US-08-
4 SerHisLeuIle.IleTyrPheLeuLeuAlaValIleGlnPheLeuLeuG 20
20 lyIlePheThrAsnGlyIleIleValValValAsnGlyIleAspLeu 35 ::        :::     :::     :::     :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::       :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::
36 IleLysHisArgLysMetAlaProLeuAspLeuLeuLeuSerCysLeuAl 52 :::
52 aValSerArgIlePheLeuGlnLeuPheIlePheTyrValA 66 :::
66 snvalilevalilePhePheIle 73
74 GluPheIleMetCysSerAlaAsnCysAlaIleLeuLeuPheIleAsnGl 90
90 uLeuGlu.LeuTrpLeuAlaThrTrpLeuGlyValPheTyrCysAlaLys 106 ::::::    ::::::::::::::::::  :::
107 ValalaSerValargHisProLeuPheIleTrpLeuLysMetArgIleSe 123    :::::::    6243CCATTCTTCTATGG
123 rlysleuValProTrpMetIleLeuGlySerLeuLeuTyrValS 138
SS
155 PheLeuargLysPhePheSerGlnAs 163
163 nAlaThrIleGlnLysGluAspThrLeuAlaIleGlnIlePheSerPheV 180
rval     
192PheAlaValLeuLeuLleDheSerLeuGlyArgHisThrar 206
, 206 gGlnMetArgAsnThrValAlaGlySerArgValProGlyArgGlyAlaP 223

HISCYSMET
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; NAME/KEY:
; LOCATION:
US-08-056-200-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-510-332-1 x US-08-056-200-93/rev
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Quality:
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Ratio: 0.774
Percent Similarity: 49.458
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NAME/KEY:
LOCATION:
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY:
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                                                                                                                                                                                                                        6936 CTGGCGCAGCTG.................TTCCTCCT 6917
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                                                                                                                                                                                                                                                                                                                                                                           7005 ......CACTTTCTGTTCCTCTAAACGGAATTTTCTGTCA 6972
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6816 GTGCAGCTGCTGCTCCTCGAGGAATTTTCTCTCTGGTTCCTGACTGC 6767
                                                                                                                                                                                                                                                          140 IleCysValPheHisSerLysTyrAlaGlyPheMetValProTyrPheLe 156
                                                                                                                                                                                                                                                                                                                           123 erLysLeuValProTrpMetI1eLeuGlySerLeuLeuTyrValSerMet 139
                                                                                                                                                                                                                                                                                                                                                                                                               106 svalAlaSerValArgHisProLeuPheIleTrpLeuLysMetArgIleS 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 LysMetAlaProLeuAspLeuLeuLeuSerCysLeuAlaValSerArgIl 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 uLeuAlaValIleGlnPheLeu.....LeuGlyIlePheT 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 leGluPheIleMetCysSerAlaAsnCysAlaIleLeuLeuPheIleAsn 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LeuGluSerHisLeuIleIleTyrPhe.....Le 11
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1645..2511
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1507..1644
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2512..8070
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Percent Identity: 23.827
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TION: 1645	
: int	
NAME/KEY: CDS LOCATION: 15071644	
; ANTI-SENSE: NO ; FEATURE:	
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; TOPOLOGY: Linear	
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CHARACTERISTICS:	
: THEORMATION FOR SEO ID NO: 93:	
TELEPHONE: (714	
; REFERENCE/DOCKET NUMBER: NIHO34.0015	
STRATION NUMBER: 36,799	
; ATTORNEY/AGENT INFORMATION:	
- 2	
DATA:	
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₹.	
ARE: PatentIn R	
S-DOS	
TYPE: Flop	
READABLE FORM:	
; COUNTRY: U.S.A.	
CA	
port Beach	
ADDRESSEE: Knobbe, Martens, Olson & Bear	
NUMBER OF SEQUENCES:	
TITLE OF INVENTION: Mehods of Using Same	
ż	
APPLICANT: Chung	
APPLICANT: Steinert, F	
<pre>seq_documentation_block. sequence 93, Application US/08800644 ; Sequence 958752 ; Patent No. 5958752 . GENERAL THEORMATION:</pre>	
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292	
256 gPheIlePheLeuPhePheIleLeuValIle 266	
· i i	
256	
H-3 -	
euLeuSerIleLeuSerPheLeuI	
6766 GCAGITCCTGTTCGCGGAATTITCT	
206 gGlnMetArgAsnThrValAlaGlySerArgValProGlyArgGlyAlaP 223	

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alignment_block:
US-09-510-332-1 x US-08-800-644-93/rev
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; LOCATION:
US-08-800-644-93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6971 CG......CTCTTGGCGGCTCAGCTGCTGTTCCTCCCTCTC 6937
                                                                                                                                                                                                                                                                                                 173 laIleGlnIlePheSerPheValAlaGluPheSerValProLeuLeuIle 189
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                                                                                                                                                                                                                                                                                                                                                                                            156 uArgLysPhePheSerGlnAsnAlaThrIleGlnLysGluAspThrLeuA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 erLysLeuValProTrpMetIleLeuGlySerLeuLeuTyrValSerMet 139
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rolleSerAlaLeuLeuSerIleLeuSerPheLeuIleLeuTyrPheSer 239
                                                                                                                                                                                           PheLeuPheAlaValLeuLeuIlePheSerLeuGlyArgHisThrAr 206
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                                                                                                                                                                                                                                                       GGCGCAGCTGCTGCTGCTGGAGGAATTTTCTCTGCCGTTGCTGCCG 6817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IleCysValPheHisSerLysTyrAlaGlyPheMetValProTyrPheLe 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGAATTTTCTGTCGCGGTCGTGACG.....CAGCTGTTGTTCGCGCTC 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .....CACTTTCTGTTCCTCTAAACGGAATTTTCTGTCA 6972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysMetAlaProLeuAspLeuLeuLeuSerCysLeuAlaValSerArgIl 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hrAsnGlyIleIleValValValAsnGlyIleAspLeuIleLysHisArg 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
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2512..8070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1
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; NAME/KEY: CDS; LOCATION: 959..184; OTHER INFORMATION: US-08-137-175A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/2/1na/5A_COMB.seq:US-08-137-175A-7
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                                                                                                                                                                                                                                                                                                                                   TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                        FEATURE:
                                                                                                                                            FEATURE:
                                                                                                                                                                                                                              MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: BAI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US92/08972
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, Iver P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 41.
STREET: Washington
CITY: Washington
CTATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: HANSSON, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256 gPheIlePheLeuPhePheIleLeuValIle 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                     OTHER INFORMATION:
                                                                                                      NAME/KEY:
                                                                                                                                                                                        ORGANISM: Borrelia burgdorferi
STRAIN: Ip90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/OFFILING DATE: 26-OCT-1993 CLASSIFICATION: 424
                                                                                                                                                         INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                  ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EE: BROWDY AND NEIMARK
419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                1958 base pairs
                                                                                                                                                                                                                                                                                                                                                                                         202-628-5197
202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HANSSON, Lennart
VENTION: IMPROVEMENT IN BORRELIA BURGDORFERI AND
VVENTION: PROPHYLAXIS
                               CDS
959..1843
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BERGSTROEM, Sven
                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                              single
                                                                                                      .949
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                                                                                    /product= "OspA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/137,175A
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alignment\_scores

202-737-3528 8633 RSEQ ID NO: RACTERISTICS: 958 base pair lieic acid SS: single linear E: CDNA RCE: Borrelia bur P90 ISOLATE: IS	CURRENT APPLICATION NUMBER: US/08/479,017  PILING DATE: CLASSIFICATION NUMBER: US/08/137,175  PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/137,175  FILING DATE: 26-CCT-1993 APPLICATION NUMBER: PCT/US92/08972  FILING DATE: 22-CCT-199 ATTORNEY/AGENT INFORMATION: NAME: COOPER, IVET P. REGISTRATION NUMBER: 28,005 REFERENCE/DOCKET NUMBER: BARBOUR-1B TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197	CORRESPONDENCE ADDRESSEE: BROWDY STREET: 419 Seven CITY: Washington STATE: D.C. COUNTRY: USA ZIP: 20004 ZIP: 20004 COMPUTER READABLE FO COMPUTER TEMPO COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: PAtenti	eq_documentation_block: Sequence 7, Application US/08479017 Sequence 7, Application US/08479017 Sequence 7, Application US/08479017 Patent No. 6143872 GENERAL INFORMATION: APPLICANT: BERGSTROEM, Sven APPLICANT: HANSSON, Lennart TITLE OF INVENTION: IMPROVEMENT IN BORRELIA BURGDORFERI TITLE OF INVENTION: PROPHYLAXIS NUMBER OF SEQUENCES: 22	195 AGGCTGCTAACATTTTGCTTACATGCTATICATGCTAATGCTAATGCTAATGCTAATATTACACCTAL 149 269 yrProSerGlyHisSerLeuIleLeuIleLeu 279 31   1   3   1   1   3   1   1   1   1	20ArgGlyAlaProIleSerAlaLeuLeuSerIleLeuSe 32 CCGTTGTTTTTATCAGAAGTTCCTTTAAGCTCAAACCTTGTCTACAACCTAGT 33 CCGTTGTTTTTATCAGAAGTTCCTTTAAGCTCAAGCTTGTCTACTTTCATTAC 34 CATTAGACTGTATTTACCATCTTTGTCTTTCTTTACTTACAAA 49 SerLeuLysPheHisIleArgArgPheIlePhe 49 SerLeuLysPheHisIleArgArgPheIlePhe 49 SerLeuLysPheHis
from			(FERI AND		Se 232 SC 290 SC 290 PA 246 PA 246 CA 196 CA 196 PA 146

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; LOCATION: 125..949
; OTHER INFORMATION: /product= "Ospa"
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; NAME/KEY: CDS
; LOCATION: 959..1843
; OTHER INFORMATION: /product= "Ospb"
US-08-479-017-7
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US-09-510-332-1 x US-08-479-017-7/rev
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Quality:
Ratio:
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Ratio: 0.611
Percent Similarity: 48.997
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                                 165 hrIleGlnLysGluAspThrLeuAlaIleGlnIlePheSerPheValAla 181
                                                                              550 TCCATTTGCTCTTACTATTGTTTTTTCAGATGCTTCACCCTTTGCGTTGA 501
                                                                                                                                                                                     136 TyrvalSermetIleCysValPheHisSerLysTyrAlaGlyPheMetVa 152
                                                                                                       644 CAGCAGCTAGAGTTCCTTCAAGAGCCAAAGTCTTTTAAAAACTTCTTTAGCT 595
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                                                                                                                                                                                                                                                                                                                        694 TTTGCTTAAAACAACAGTGCCTTCTGTAACTTTTAATGTTGTTTTTGCCGT 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             817 TCGGCTATTCACACTAATTGTTAAAGTGGAAGTCTTTGAATCCCATGTTC 768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               955 CTCTCCCTATTTTAAAGCATCTTTAAGTTCTTTAAGCGTTGTAATTTCGA 906
                                                                                                                                                                                                                                                                                                                                                                                                                                       86 uPheIleAsnGluLeuGluLeuTrpLeuAlaThrTrpLeuGlyValPheT 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 IlePhePheIleGluPheIleMetCysSerAlaAsnCysAlaIleLeuLe 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 yr.....ValAsnValIleVal 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 ePhe.....LeuGlnLeuPheIlePheT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 LysMetAlaProLeuAspLeuLeuLeuSerCysLeuAlaValSerArgIl 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 lyIleAspLeuIleLysHis......Arg 39
                                                                                                                                                            TTT...CCGGTTTTATCGCTTTTTATGTCTGTGTATTCAAGT...CTGGT 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 349
Gaps: 21
Percent Identity: 23.496
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		6	
		5-8550 (0176 (0: 13: (CS: pairs	INF
٠		ION: 29,655 ER: NIH121.001CP1 MATION:	ORNEY/AGENT INFORMA AME: ISraelsen, Ne EGISTRATION NUMBER: EFERENCE/DOCKET NUM ECOMMUNICATION INFO
		US/08/487,826B 1993	APPLICATION N FILING DATE: CLASSIFICATIO
		PC-DOS/MS-DOS Release #1.0, Version #1.25 ATA:	OPERATING SYSTEM: SOFTWARE: PatentI CURRENT APPLICATION
		RM: py disk compatible	COMPUTER READABLE FO MEDIUM TYPE: Flog COMPUTER: IBM PC
			STATE: Califor COUNTRY: US
		irtens Olson & Bear Center Drive 16th Floor	ADDRESSEE: Knobbe STREET: 620 Newport
PROTEINS	BINDING	5	NUMBER OF SEQUENCES: CORRESPONDENCE ADDRES
		mas E.  DING DOMAINS FROM PLASMODIUM VIVAX	APPLICANT: Wellems, TITLE OF INVENTION:
		David S.	APPLICANT: Peterson APPLICANT: Su, Xin-
		m	APPLICANT: Sim, Kim APPLICANT: Chitnis,
		US/08487826B	<pre>seq_documentation_block:     Sequence 13, Application     Patent No. 5993827     GENERAL INFORMATION:</pre>
		/2/ina/5B_COMB.seq:US-08-487-826B-13	seq_name: /cgn2_6/ptodata/2
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		LeuPhePheIleLeuValIleGlyIleT 269	260
		euLysPheHisIleArgArgPheIlePhe 259                	249 SerLeuLysPheHis :::            245 GAACTTGCATTCCACCAG
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		rgAsnThrValAlaGlySerArgValProGly 219	203 rghisthrargoinmetargashthrValAlaG
		AGTT	CTC
		IlePheLeuPheAlaValLeuLeuLeuIlePheSerLeuGlyA 203	189IlePheLeuPl
		AATGTTTTGCCATCTTCTTGAAGATTTCAAATGTGGTTTTACTTAGATC 401	
		Serval ProLenie	182 GIUPNE

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alignment_block:
US-09-510-332-1 x US-08-487-826B-13
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17546 TGTTAATAATAAAAAGGAGATTTTCGAAGAGGAATATCCTATATCAGATA 17595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17496 ACTAATAATAATATGGATGTACCTACTAAAATGCACATCGAAATGAATAT 17545
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MOLECULE TYPE: cDI
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17925
                                                                                                                      17960 CTAATATATATCCTTCTATTTTCGATTTTTTCATTTTTTCCAGTATT
                                                   18010
                                                                                                                                                            174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 spLeuIleLysHisArgLysMetAlaProLeuAspLeuLeuLeuSerCys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 eLeuLeuGlyIlePheThrAsnGlyIleIleValValValAsnGlyIleA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92 uLeuTrpLeuAlaThrTrpLeuGlyValPheTyrCysAlaLysValAlaS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MetLeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIleGlnPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CysSer...AlaAsnCysAlaIleLeuLeuPheIle...AsnGluLeuGl 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuAlaValSerArgIle......PheLeu......GlnLeu.P 61
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                                                                                                                                                                                                                                                                    TATGTATATTATGGTTATTTTGTTTTCTGTACATTTTTCGTAA 17924
                                                                                                                                                       IleGlnIlePheSerPheValAlaGluPhe.....SerValProLeuLe 188
                                                                                                                                                                                               TATATATAT.....
                                                                                                                                                                                                                                                                                                                                       .....TTTTATTTTTAGTATAATAATTGTATCTATATTTGATTAATAA 1787
                                                                                                                                                                                                                                                                                                                                                                       ValProTrpMetIleLeuGlySerLeuLeuTyrValSerMetIle..... 140
                                               .CysValPheHisSerLysTyrAlaGlyPheMetValProTyrPheLeuA 157
                                                                                      uIlePheLeuPhe.....
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               AlaValLeuLeuIlePheSerLeuGlyArgHisThrArg 206
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Percent Identity: 21.148
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seq_name: /cgn2_6/ptodata/2/ina/6_COMB.seq:US-08-748-506-9
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US-08-748-506-9
                                      alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18101 CTAATTCTGAATAATCCGAGCGAAAAAAAAATATATATCTC.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18060 TITATATATGTGTTTTATATGTGTTTTATTTTT......GTTACT 18100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18242 AATTTCTTATTTTATTTAACTTTATTCCTTTTTAATTTCTTAATTCTT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18339 АЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАТТАТТАТАТАТАТАЛАТАЛА 18377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 Lysphe.HisIleArgArgPheIlePheLeuPhePheIleLeuValIleG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 GlnMetArgAsnThrValAlaGlySerArgValProGlyArgGlyAlaPr 223
                                                                                                                                                                                                                                TELEFAX: 312-616-5700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 LeuLysGlnAsnAlaLysLysPheLeuLeuHisSerLys 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NOVEL SPERM RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 74
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Two Pr
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 60601-6780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 08-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                    TELEPHONE:
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                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                           LENGTH:
Quality:
Ratio:
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Two Prudential Plaza, Suite 4900
                                                                                                                                                                                         984 base pairs
                                                                                                                                                                                                                                                  312-616-5700
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                                                                                                                                      Tinear
                                                                                                                                                                                                                                                                        312-616-5600
    103.50
0.690
                                                                                                                  DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #
        265
12
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-153-848-39
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US-09-510-332-1 x US-08-748-506-9
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                                                             754
                                                                                             246 PheLeuSerSerLeuLysPheHisIleArgArgPheIlePheLeu 260
                                                                                                                                                                                               229 erileLeuSerPheLeuIleLeuTyrPheSerHisCysMetIleLysVal 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 elleTrpLeuLysMetArgIleSerLysLeuValProTrpMetIleLeuG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          373 TCCCTGGACCGCTTTCTGGCCATCTGCAAACCTCTACATTATCCAACCAT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 GlyVal...PheTyrCysAlaLysValAlaSerValArgHisProLeuPh 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          323 TCGTCTATCTTGTCGTGGGGCCAACAGGTTTTTTCCTTTTGGCTGCGTTA 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            273 TCTGTCAGGGAGGCAAAAGATTCCCTTTGGGGTCTGCTTCTCACAGGCCT 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 ..CACCGACTGCAGACGCCCATGTACTTCTTCTCAGCACCTTCTCTTT 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 CCTCATGGGCAACATGCTCATAATTACCATCACCTGTGTGGAC..... 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83 lalleLeuLeuPhelleAsnGluLeuGluLeuTrpLeuAlaThrTrpLeu 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 lilePhe.......PheileGluPheileMetCysSerAlaAsnCysA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 ValSerArgIlePheLeuGlnLeuPheIlePheTyrValAsnValIleVa 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 ysH1sArgLysMetAlaProLeuAspLeuLeuLeuSerCysLeuAla... 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 yIlePheThrAsnGlyIleIleValValValAsnGlyIleAspLeuIleL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 CACCTGAAGATCCTCTTCTTCCTACTGCACTTGCTGGCCTACTTGGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 HisLeu...IleIleTyrPheLeuLeuAlaValIleGlnPheLeuLeuGl
                                               ATTGTCCTCTCTAATGTATGGCAGCTGTGCATTTATATACCTG 798
                                                                                                                                                                                                                                                 CACCATAGTGAGACTCCCTTCAGCCAGGGAGCGACAGAGAGCT.....
                                                                                                                                                                                                                                                                                                 lAlaGlySerArgValProGlyArgGlyAlaProIleSerAlaLeuLeuS 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nAsnAlaThrIleGlnLysGluAspThrLeuAlaIleGlnIlePheSerP 179
                                                                                                                                                                                                                                                                                                                                                 ATAGCCATCTTTGCATACAGC.....AATATAGTAGT 686
                                                                                                                                                                                                                                                                                                                                                                                                    LeuLeuIlePheSerLeuGlyArgHisThrArgGlnMetArgAsnThrVa 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         heValAlaGluPheSerValProLeuLeuIlePheLeuPheAlaValLeu 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TACTGTGGTCCAAACATTATTCCTCACTTTTTCTGTGAT...TTTGGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TyrAlaGly...PheMetValProTyrPheLeuArgLysPhePheSerGl 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTTCCTCTCATGGCCAGTCCAGTT...GTGATGCTTTCCAAGACATTT 519
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                                                                                                                                                  .....TTTACCCTTGCTGTAATTGTGCTTTTTGCTTCCTTTCTT 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGGAGTGTTGTTTTATAACTACTGCTATCCCCCAGCTCCTCACCATCAT 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity: 22.264
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alignment_scores:
Quality:
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TELEPHONE: (312) 474-0448
TELEX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 39
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
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; Sequence 39, Application US/08153848
; Patent No. 5759804
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                                   383 GGCGCTCAGCTGATATCTTCATTGCTAGCCTGGCGGTG.......420
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                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
APPLICATION NUMBER: US 07/977,452
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 31,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTED:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE:
FILING DATE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
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                                                                         41 etAlaProLeuAspLeuLeuLeuSerCysLeuAlaValSerArgIlePhe
                                                                                                                                                     24 nGlyIleIleValValAsnGlyIleAspLeuIleLysHisArgLysM 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
58 LeuGlnLeuPheIlePheTyrValAsnValIleValIlePhePheIleG1 74
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APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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CITY: Chicago
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oLysLeuLys(	CAGCTACGTCAAC	PhePheI     rgrgaCTTTGACC	heHisIleArgAr ::   ::: accaccTGGTGAA	LeuTyrPheSer :::     ::: GTGACCTTTGCC	lyArgGlyAlaP     GCCGG	yArgHisThrAr :        TGGCCACTTCCG	ProLeuLeuIleP    :::    :  CCCTTCACCATCA	hrLeual :: :: :::	rPheLeuArgLys :::::: CTACATGGAC	PheHisSerLysT ::: ATGGTGTTACGCA	alProTrpMetIle     TGGCCACGGCAGTT	ValArgHisPrc        GTGAGGCCAGTG	CCAGCGTCTTCT	yValPheTyrCy  :::   :::   GACCTTCTTCTG	GluLeuTrpLeu         CCCCTGTGG	helleMetCysS	
31nAsnAlaLysLy.     ::: ::	SerGlyHis ::: AGCTGCCTCAAC	::leLeuValIleGl :::::::::::::::::::::::::::::::::::	:gArgPheIlePheLeu ;;; ;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;	HisCysMetIleL      CTGTGCTGG	SerAlaLe    CI	gGlnMetArgAsn  :::  CAAGGAACGC	heLeuPhea: ::    :TGCTGACCT	AlaIleGlnIlePhe :::::: GCCTTGGGGTCTCG	PhePheSe:::    :::    TACTC	yrAlaGlyPheM :::    .CCACCGGGGACT	LeuGlySerLe      TTTGGGTGCT	)LeuPheIleTrpLeu      GCCAATGCTCGGCTO	GCCTCACCGGCCT	S    CAAGCTCAGCAGC	AlaThrTrp      ::: GCTACCTACACGT	erAlaAsnCysAl    GC	
aLysLysPheLeuLeuHi : :::::    caccrccargcrc	SerLeuIleLeu :::::: CCCTTCCTCTAT	yIleTyrPro. :   :::    CATCTTCCCCT	CTGGGCAGCCT	. 🔾	uLeuSerIleL            GCTCAGCATCA	ThrValAlaGl :::    ATCGAGGG	lavalLeuLeuLeuI ;; ;;;;;; ;;TACTTCTTCATCG	Vala :::: CACCG	rGlnAsnAlaThrIle  :::        ::: caTGGTGGCCACTGTG	et :: TGGAGAACACC <i>I</i>	PuLeuTyrValSe     GGCCGCCCTCCT	LysMetArg  :::::     AGGCTGCGG	GCTTC	TACCTCATCTT	PACCGGGACTATG	AlaIleLeuLeuPh           GCTGACCTGACCTT	:
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s 298     1179	P 282    C 1141	. 270 T 1091	. 260 C 1041	252 F 991	962	218	202	185 836	170 786	154 742	142 692	125 642	109 592	104 542	99 492	91 445	420

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Database: N_Geneseq_36:*
Database sequences: 480022
Database length: 187831343
Search time (sec): 75.850000
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Query: US-09-510-332-1
Query length: 299
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/cgn2_2/gcgdata/geneseq/geneseqn/NA1994.DAT:G62924
The PNS and proteins of the invention are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, hematopoiesis regulating activity, tissue growth activity, hemostatic activity, chemostatic/chemokinetic activity, hemostatic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumor invasion suppressor activity, and tumor inhibition activity. The PNS are also stated to be useful for gene therapy. Other activities include inhibiting the growth, infection or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polynucleotide sequence of the pt127_1 clone
                                                                                                                                                                                                                                                                         Claim 26; Page 113-114; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides encoding human secreted proteins used therapeutic, diagnostic and research purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_2/gcgdata/geneseq/geneseqn/NA1999.DAT:z20861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   n; cDNA library; clone; transmeml cloning; hybridization cloning;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers 1129..1899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_except=
1150..1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LaVallie ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vallie ER, Collins-Racie LA,
Steininger RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pt127_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (pos:1318..1320,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transmembrane cloning; gene
                                                                                                                                                                                                                                                                         acid sequence of the encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106.
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106.
106.
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143
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                                                                                                     hemostatic
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0.5999
27.43
3.29
3.54
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function of bacteria, fungi, viruses and other parasites; effecting bodily characteristics such as, e.g. weight, color, skin, etc., effecting biorhythms or circadian cycles; enhancing fertility; treatment of depression; treatment of pain; hormonal or endocrine activity.

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alignment_scores:
Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: 220861 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-510-332-1 x 220861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                              1615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1379 CTATTAATGCCTGGGCTGTAACCAACCATTTCAGCATCTGGGTTGCTACT 1428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1197 TAATGGCTTCATAGTGTTGGTAAATTCCATTGAGTGGGTCAAGAGACAAA 1246
                                204 sThrArgGlnMetArgAsnThrValAlaGlySerArgValProGlyArgG
                                                                                                                                                                               171 hrLeuAlaIleGlnIlePheSerPheValAlaGluPheSerValProLeu 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1247 AGATCTCCTTTGCTGACCAAATTCTCACTGCTCTGGCAGTCTCCAGAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2695 BP; 858 A; 427 C; 486 G; 919 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 ysMetAlaProLeuAspLeuLeuSerCysLeuAlaValSerArgIle 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 rAsnGlyIleIleValValValAsnGlyIleAspLeuIleLysHisArgL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 IleIleTyrPheLeuLeuAlaValIleGlnPheLeuLeuGlyIlePheTh 23
TCTCAAGAAGATG......CAGTTCCATGCCAAAG
                                                                     ACTCTGTCCCTGTTATCTTTTCTGCTCTTAATCTGTTCTTTTGTGTAAACA
                                                                                                      LeuIlePheLeuPheAlaValLeuLeuLeuIlePheSerLeuGlyArgHi
                                                                                                                                                                                                                                                                                          ATGGATGAGAGTATGTGGACAAAAGAATATGAAGGAAACGTG..... 1614
                                                                                                                                                                                                                                                                                                                                                               ACCTTTCAGATATGACTGTAACCACGCTTGCAAACTTA...ATACCCTTT
                                                                                                                                                                                                                                                     rPheLeuArgLysPhePheSerGlnAsnAlaThrIleGlnLysGluAspT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                uPheIleTrpLeuLysMetArgIleSerLysLeuValProTrpMetIleL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCAACTGTTTTGAATCCAGGTTCATATAGTTTAGGAGTAAGAATTACTA 1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTTTG.....CTCTGGGTAATATTATWACATTGGTA 132
                                                                                                                                                                                                                                                                                                                            .....ValPheHisSerLysTyrAlaGlyPheMetValProTy 154
                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTTCTTCACTTAAAAAGGAGAATTAAGAGTGTCATTCCAGTGATACTAT 1528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TrpLeuGlyValPheTyrCysAlaLysValAlaSerValArgHisProLe 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....AsnGluLeuGluLeuTrpLeuAlaThr 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eGluPheIleMetCysSerAlaAsnCysAlaIleLeuLeuPheIle....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PheLeuGlnLeuPheIlePheTyrValAsnValIleValIlePhePheIl 73
                                                                                                                                                                                                                      ·····AGTTGGGAGATCAAATTGAGTGATCCGACGC
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1.669
59.259
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Gaps: 11
Percent Identity: 29.938
 1771
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seq_documentation_block:
ID V62130 standard; DNA; 8952 BP
XX

AC V62130;

XX

DT 07-DEC-1998 (first entry)
XX

HSV-2 strain SB5; immunologic
KW HSV-2 strain SB5; immunologic
KW antiviral identification; vir
XX

FH Key Location/Qual
FT CDS Location/Qual
FT CDS Location/Qual
FT CDS 1372.4017
FT CDS 1372.4017
FT CDS 1372.4017
FT CDS 4084.4689
FT CDS 4084.4689
FT CDS Complement (4
FT CDS 7489-6
FT CDS 7489-6
FT CDS 7489-6
FT CDS 7589-6
FT CDS 75970duct-70R
FT CDS 7590duct-70R
FT 75
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      (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2007 GATTTTGTGTCAGATTAAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSV-2 strain SB5; immunological response induction; therapy; antiviral identification; viral protein inhibitor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Herpes simplex virus type 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSV-2 strain SB5 Contig ID 100 DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           290 sPheLeuLeuHisSerLysCys 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221
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                                                                                                                                                                                                                                                                                                                                         /*tag= e
/product= "ORF#5 protein"
/product= "ORF#5 protein"
/product= "ORF#5 protein"
/*tag= f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (5646..6650)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= c
/product= "ORF#3 protein"
complement (4889..5407)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "ORF#1 protein"
/transl_except= (pos: 1..2, aa: Ala-Xaa)
/note= "Xaa= unspecified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers complement (1..1802)
                                                                                                                                                                                                                                                                                                                                      /product= "ORF#6 protein'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "ORF#4 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "ORF#2 protein'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВP
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alignment_scores
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US-09-510-332-1 x V62130
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: V62130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a Herpes simplex virus type-2 (HSV-2) DNA sequence of the invention. This sequence was isolated from HSV-2 strain SB5 (deposited as ATCC VR-2546), is designated Contig ID 100, and encodes 6 HSV-2 proteins. The proteins can be used for the treatment or prevention of disease, to induce an immunological response in a mammal or to identify inhibitors, activators or novel antivirals. Antagonists of the proteins can be used to inhibit a viral polypeptide. The DNA sequence or a vector containing it can also be used to induce an immunological
                                                                                                                                                                                                                                                                                                                                                                                                            8021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herpes simplex virus type-2 sequences – useful in, e.g. prevention and treatment of infection or inducing immunological response in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chan JY,
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P-PSDB; .W72001, W72002, W72003, W72004, W72005, W72006
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142 lPheHisSerLys...
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                                                                                                                                                                                                                                                                                                                                                                   87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITCTTCCTCTCT.....CTTTTCTTCTCCTCCTCCTATCCTCTTATC. 7982
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ephepheIleGluPheIleMetCysSerAlaAsnCysAla.IleLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerArgIlePheLeuGlnLeuPheIlePheTyrValAsnValIleValIl 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :::|||||| |||||:::|||||||| 8012
                                                                                                                                                                                                                                                                     rCysAlaLysValAlaSerValArgHisProLeuPheIleTrpLeuLysM 120
                                                                                                                                      TCATTCTTTCTCTACTC......ACGTTACTCTAT 8157
                                                                                                                                                                             etArgIleSerLysLeuValProTrpMetIleLeuGlySerLeuLeuTyr 136
                                                                                                                                                                                                                          CTGT.....CACTCTATCTCTTTTCCCTTCTTTTATATGTGTCGTAT 8128
                                                                                                                                                                                                                                                                                                                                                              PheIleAsnGluLeuGluLeuTrpLeuAlaThrTrpLeuGlyValPheTy 103
                                             ValSer.....MetIleCysVa 142
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0.878
44.037
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  .....TyrAlaGlyPheMetValProT 154
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Identity:
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16
22.630
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seq_documentation_block:
ID Q87587 standard; DN
                                                                                                                                                                                                                                                                                                                                                                               seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1995.DAT:Q87587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8208 TCTCTCTTCCTTTTCCTTTAATATATTTTCTTTTACTCATCCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8258' TTTTCACTTTACTATTCCAT.............
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8532 CTCTCTCCTCTGCTCACACTTACTTCCTCCTCCTCCCAATTTGTCTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 yrpheLeuArgLysPhePheSerGlnAsnAlaThrIleGlnLysGluAsp 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189
                                                                                                                                                                                                                                                                                                                                                                                                            8582 CGTCTCTCACTCTTCTCCTTTCTCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218 oGlyArgGlyAlaProIleSerAlaLeuLeuSerIleLeuSerPheLeuI 235
                                                                                                                                                                                                                                                              DNA encoding Leucocytozoan protozoa structural protein epitope
                                                                                                                                                                                                                                                                                          19-DEC-1995 (first entry)
                                                                                                                                             04-APR-1995
                                                                                                                                                                       JP07089995-A.
                                                                                                                                                                                              Leucocytozoan
                                                                                                                                                                                                                         leucocytozoan protozoa; structural protein; epitope; vaccine; fowl; leucocytozoanosis; treatment; ss.
                          WPI; 1995-167252/22
                                                  (DOBU-) DOBUTSUYO
                                                                                                                   10-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aGluPheSerValProLeuLeu...........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ThrLeuAlaIleGlnIlePheSer.....PheValAl 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlyArgHisThrArgGlnMetArgAsnThrValAlaGlySerArgValPr 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PheHisIleArgArgPheIlePheLeuPhePheIle.LeuValIleGlyI 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCTC...ATATCTCACCTCTCGTTC.......TCTCCCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leLeuTyrPheSerHisCysMetIleLysValPheLeuSerSerLeuLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....IlepheLeupheAlaValLeuLeuIlepheSerLeu 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCACTTTCTCCCTCCTCCACTCTTCTCATCTTTTTTTTCTCTACTCAACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .........GTGTATCTCTTCTCTCTTTTTTTCTCTCTCTTTATTTC 8318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LysGlnAsnAlaLysLysPheLeuLeu 293
                                                                                                                                                                                                 protozoa sp
                                                                                          93JP-0226078
                                                                                                                    93JP-0226078
                                                                                                                                                                                                                                                                                                                                              DNA; 1686 BP
                                                    SEIBUTSUGAKUTEKI SEIZAI KYOKAI.
KK.
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232

737 216 757 200 807

708

564 274 809 257 658 243

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alignment_block:
US-09-510-332-1 x Q87587/rev
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Quality:
Ratio:
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Ratio: 0.801
Percent Similarity: 48.297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to reverse of: Q87587
                                                                                                                                                                                                                                                                                                                                                               1063
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1363 CTTCTATCATTTCTTCAACTACTGGTGTTTCTTCTACTACTTCTTCA 1314
172 LeuAlaIleGlnIlePheSerPheValAlaGluPheSerValProLeuLe
                                                                                                                                                                                                                                                105 aLysValAlaSerValArgHisProLeuPheIle.TrpLeuLysMetArg 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q87587-89 encode polypeptides having a whole or partial epitope of structural protein of Leucocytozoan protozoa (see R70491-93). The polypeptides and DNA encoding them are useful in the production of vaccines for the treatment of leucocytozoanosis of fowl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1686 BP; 915 A; 129 C; 382 G; 260 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 12-14; 20pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immune inducing polypeptide against Leucocytozoan protozoa - Immune inducing polypeptide against Leucocytozoan protozoa - Immune inducing polypeptide against Leucocytozoanosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38
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                                                                                                 TTTTGTTCATTTGTTTTTCCTTGTACTTGTCCATTTTGTT.....
                                                                                                                                                                                              IleSerLysLeuValProTrpMetIleLeuGlySerLeuLeuTyrValSe 138
                                                                                                                                                            ATGACCAAATTG......891
                                                                                                                                                                                                                                                                                         TCGGATTTTGATTCA...TTAGTTACT...TTAATGTTATAATTTTGCTG 970
                                                                                                                                                                                                                                                                                                                         AsnGluLeuGluLeuTrpLeuAlaThrTrpLeuGlyValPheTyrCysAl 105
                                                                                                                                                                                                                                                                                                                                                         ATGATGAATTTTTATTTTCATCTTCAAATATATTTGTAGTTGAATTTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTACAGGTGTTTCTATCATTTCTTCTTCAACTACAGGTGTTTCTTCT 116
                                                                                                                                 rMetIleCysValPheHisSerLysTyrAlaGlyPheMetValProTyrP 155
                                                                                                                                                                                                                              ATTAGTTTTTTCTGTTTCTGTTCTTTTATTTATCATATATCTTAATATTG 920
                                                                                                                                                                                                                                                                                                                                                                                                                       TGGTCCGGAATTCCGGCCTCTAGTAGCTTCATTTAATTCTGGTTTTTTCA 1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ile..GluPheIleMetCysSerAlaAsnCysAlaIleLeuLeuPheIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCATTTCTTCAACTACTGGTGTTTCTTCAACAACTTCTTCAACTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....ValAsnValIleValIlePhePhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....AspLeuLeuLeuSerCysLeuAlaValSerArgIlePhe.... 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .....LeuGlnLeuPheIlePheTyr.......
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Gaps: 18
Percent Identity: 25.077
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in
      seq_documentation_block: ID T17115 standard; DNA; 3016 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1996.DAT:T17115
                                                                 mutation
                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                      5'UTR
                                                                                                                                                                                                                                                                                                                                                                    Key
5'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; rhodopsin; transversion; mutation; retinitis pigmentosa; probe; primer; hybridisation; polymerase chain reaction; PCR; eye; rod; retina; diagnostic; prenatal diagnosis; photoreceptor;
                  primer_bind
                                                                                                                              misc_binding
                                                                                                                                                                                            misc_binding
                                                                                                                                                                                                                                                                                         primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhodopsin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUL-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T17115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IlePheLeuPhePheIleLeuValIleGlyIleTyrProSerGlyHisSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTCATCTTTTTCTTTTCAACATATATTTTTCATCTTCTTGTTCTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           leLysValPheLeu...SerSerLeuLysPheH1sIleArg...ArgPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ....PheLeuIleLeu......TyrPheSerHisCysMetI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTTTTTCTAATTCTTTAAAATGTTCTTGTTCTTTTTCTACATATACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             erLeuGlyArgHisThrArgGlnMetArgAsnThrValAlaGlySerArg
|||||:::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTTTTACTTCTGATTTTTCTCATCTA.....TTTCTTCTGATTCTCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ......GTTCACTTTCTACTTTTCTTCTAAAACT
               /*tag= g
/note= "Substitution with A in
362..381
                                                                                                                                                                                                                                                                               /*tag= b
/note= "Alternative 5'-UTR"
complement (231..250)
                                                                                                                                                                                                                                                                                                                                    /*tag= 8
202..294
                                                                               /note= "Binds probes T17119 (normal)"
                                                                                                               complement (355..369)
/*tag= f
                                                                                                                                                                                    /product= Rhodopsin complement (354..372)
                                                                                                                                                                                                                               /*tag= c
/note= "Binds primer 348
295..5278
                                                                                                                                           Location/Qualifiers
200..294
                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         548
                                                                                                                                                                                                                                                                                                                                                       מ
                                                                                                                                                                                                                                                         (T17121)"
                                                                                            (mutant)
                                                                                                                                                          (mutant)
                              mutant sequence
                                                                                              and
                                                                                                                                                          and T17118
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ds.

T17120

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alignment_block:
US-09-510-332-1 x T17115
                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence encodes human rhodopsin, and is shown without introns. The full sequence, with introns, is shown in T17116 Substitution of histidine for the normal nonpolar amino acid proline at position 23, by substitution of C with A in codon-23, results in a dysfunctional or absent molecule, affecting rod function, and is linked with autosomal dominant retinitis pigmentosa. Probes T17117 and T17119 bind to the C-to-A representation sequence, and probes T17118 and T17120 bind to the corresponding normal sequence. Primers 485 (T17122) and 502 to the corresponding normal sequence. Primers 485 (T17121) to amplify mutant and normal sequences, respectively, by PCR. Mutations in the retinal degeneration slow protein and retinal rod cGNP-phosphodiestorase genes are also implicated in retinitis pigmentosa. Detection of any of these mutations in a foetus or
                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                        Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-MAR-1993;
24-JAN-1990;
11-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diagnosis of hereditary retinal degenerative diseases e.g. retinitis pigmentosa, - caused by a human photoreceptor protein mutation, by detection of the mutation by PCR amplification or hybridisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAR-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US5498521-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JAN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-159684/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Berson EL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3016 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Column 19-24; 71pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 patient may be used in
                                                                                                                                                                      450
                                                                                                     484
                                                                                                                                                                                                   17 eLeuLeuGlyIlePheThrAsnGlyIleIleValValValAsnGlyIleA 34
                                                                 50
                                                                                                                                                                                                                                                                       1 MetLeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIleGlnPh
                                                                                                                                                                                                                                   ATGCTGGCCGCCTACATG.....TTTCTGCTGATCGTGCTGGGCTT
                                AACCTAGCGGTGGCTGACCTCTTCATGGTCCTAGGTGGCTTCACCAGCAC
\verb|nValileValilePhePheIleGluPheIleMetCysSerAlaAsnCysA|
                                                               CysLeuAlaValSerArgIlePheLeuGlnLeuPheIlePheTyrValAs
                                                                                                                                spLeuIleLysHisArgLysMet...AlaProLeuAspLeuLeuLeuSer 49
                                                                                                                                                                      CCCCATCAACTTCCTCACGCTCTACGTCACCGTC.
                                                                                                   .....CAGCACAAGAAGCTGCGCACGCCTCTCAACTACATCCTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R93116.
                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dryja TP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93US-0033081.
90US-0469215.
91US-0805123.
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                                                                                                                                                                                                                                                                                                          T17115
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                                                                                                                                                                                                                                                                                                                                                                                             124.50
0.759
50.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  689 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis.
                                                                                                                                                                                                                                                                                                             from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  863 C; 753 G; 711 T;
                                                                                                                                                                                                                                                                                                                                                                                       Length: 328
Gaps: 16
Percent Identity: 20.732
                                                                                                                                                                                                                                                                                                             μ
                                                                                                                                                                                                                                                                                                             to:
                                                                                                                                                                                                                                                                                                               3016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0 other;
                                                                                                                                                                                                                                              449
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seq_documentation_block:
ID V21511 standard; DN
                                                                                                                                                               seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1998.DAT:V21511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                576 CCTCTACACCTCTCTGCATGGATACTTCGTCTTCGGGCCCACAGGATGCA 625
                                                                                                                                                                                                           1234
                                                                                                                                                                                                                                                                                                                                                            1154
                                                                                                                                                                                                                                                                                                                                                                                                                                    1104
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                                                                                                                                                                                                                                                                                                                  GlyHisSerLeuIleLeuIleLeuGlyAsnProLysLeuLysGlnAsnAl 288
                                                                                                                                                                                                                                                                                                                                                                                                                                  CGTGGCATTCTACATCTTCACCCACCAGGGCTCCAACTTCGGTCCCATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCATCATGGTCATCGCTTTCCTGATCTGCTGGGTGCCCTACGCCAG 1103
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus Union? The sequence of the BacRI operon of CC was determined by N-terminal sequencing of purified BacRI operon CC (see W54171), with back-translation and plasmid analysis. The BacRI operon includes the BacRI gene (see V21510), a homologue of the cylM gene of the cytolysin operon of Enterococcus faecalis. CC whose function is involved in the maturation of pre-cytolysin, CC lactococcin biosynthesis and modification, and a gene Involved in CC immunity function. BacRI peptides can be produced by construction CC of an expression vector containing an oligonucleotide or operon CC coding for BacRI, and use of the vector to transform host cells for CC plasmid publio, and Bacillus subtilis transformants secreted the CC expression. The entire BacRI operon has been cloned into CC plasmid publio, and Bacillus subtilis transformants secreted the CC expression secretical peptides can be produced by construction CC coding for BacRI, and use of the vector to transform host cells for CC sagainst many Gram-positive and Gram-negative organisms such CC staphylococcus aureus; Moraxella bovis, causing infectious bovine CC used as an anti-cancer agent.
                                                                                                                                                                          Align seg 1/1 to reverse of: V21511
                                                                                                                                                                                                           US-09-510-332-1 x V21511/rev
                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                  Sequence 6755 BP; 3903 A; 1252 C; 1600 G;
79 erAlaAsnCysAlaIleLeuLeu.....PheIleAsnGluLeuGluLeu
                                                                  62 ePheTyrValAsnValIleValIlePhePheIleGluPheIleMetCysS 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Therapeutic proteinaceous substances from Staphylococcus aureus - useful to inhibit growth of wide range of prokaryotic or eukaryotic cells, e.g. Moraxella bovis causing infectious bovine keratoconjunctivitis
                                                                                                                                             48
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19-SEP-1996;
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Ratio:
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ID T69547 standard; DNA; 1496
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                      W09714790-A1
                                                                                                              CDS
                                                                                                                                                                                                                                                  Pheromone receptor; vomeronasal sensory neuron; social behaviour; maternal behaviour; reproductive behaviour; fertility; hormone secretion; ss.
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alignment_scores:
Quality:
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US-09-510-332-1 x T69547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              c cDNA clones (T69546-50) respectively code for rat pheromone receptors VN3, VN4, VN5, VN6 and VN7 (WJ9104-08), members of a covel family of presumed 7-transmembrane domain receptors that are covolutionary independent of the odorant receptors of the main colfactory epithelium. These clones, and a clone for VN2 (sequence not provided), were isolated from rat vomeronasal organ cDNA (libraries by PCR and hybridisation. A differential cloning method was used to isolate VN7 cDNA (T69545). VN1-VN7 (not VN2) clones have been deposited in pBluescript as ATCC 97294-97299. A human homologue, HG25 (T69551), has also been isolated. VN polypeptides can be expressed in host-vector systems for use in identifying modulators for control of maternal, reproductive and social behaviour, to increase fertility, control hormone secretion and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: T69547 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid molecule encoding vertebrate pheromone receptor useful to identify modulators for control of reproductive and social behaviour, fertility and hormone secretion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-OCT-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 10; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1496 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               behaviour, to increase fertility, control in regulate food uptake in humans and animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                         417 GTTGGCATCTTAGCTAACAGTATCCTGTTTTTTGGTCACCTGTGCATGCT
                                                                                                                                                                                                                                                                                  517
                                                                                                                                                                                                                                                                                                                                                             467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 LeuGlyIlePheThrAsnGlyIleIleValValValAsnGlyIleAspLe
                                                                                                                                                                                                                                                                                                                     52
                                                                                                                                                                                                                                                                                                                                                                                                 35 uIleLysHisArgLysMetAlaProLeuAspLeuLeuLeuSerCysLeuA 52
                                                                                                                                                                                                                                                                                                                 laValSerArgIlePheLeuGlnLeuPheIlePheTyrValAsnValIle
                                                                                                                                                                                                  GACATGTTTATTTCTCAGGGGATATGGGATTCTACCTCATGCCAGTCCCT
                                                                                                                                                                                                                                      ValIlePhePheIleGluPheIleMetCysSerAlaAsnCysAlaIleLe
                                                                                                                                                                                                                                                                                                                                                           CCTTGGAGAGAACAAGCCTAAGCCCATTCATCTCTACATTGCATCCTTGT 516
                                         TGCTGAATGTCTTTTGGATGATCACTCTCAGTTCTAAAAAATCCTGTTTA
                                                                                                                                                                                                                                                                                  CCCTAACACAACTAATGCTG...CTTATAACTATGGGACTCATAGCTGCT
                                                                                                                       TATCTATTTGCACAGGCTTTCGAGGGGTTTTACCCTTAGTGCTGCCTGTC
                                                                                                                                                        uLeuPheIleAsnGluLeuGlu.....LeuTrpLeuAlaThrT
PheIleTrpLeuLysMetArgIleSerLysLeuValProTrpMetIleLe 131
                                                                             rpLeuGlyValPheTyrCysAlaLysValAlaSerValArgHisProLeu
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54.785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 303
Gaps: 11
Percent Identity: 20.792
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DT XXX
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ID V53631 standard; cD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 uGlySerLeuLeuTyrValSerMetIleCysValPheHisSerLysTyrA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1260 TGTGCCAGA 1268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201
                                                                                                                                                              cancer; anorexia; asthma; Parkinson's disease; acute heart failure; hypotension; hypertension; urinary retention; osteoporosis; angina pectoris; myocardial infarction; ulcer; allergy; benign prostatic hypertrophy; psychosis; anxiety; schizophrenia; manic depression; delirium; dementia; mental retardation; dyskinesia; Huntingdon's disease; Gilles de la Tourette's syndrome; hypertrophy in the control of the co
                                                                                                                                                                                                                                                                                                                                                                                      HNFDY20; G-protein coupled receptor; human; infection; HIV; pain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human 7-transmembrane receptor HNFDY20 cDNA
Key
                                                                    Homo sapiens
                                                                                                                                    therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              laGlyPheMetValProTyrPheLeuArgLysPhePheSerGlnAsnAla 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCAAAGTCATCTCCAGAGCAAAGGGCCACCGAGACCATCCTGCTGCTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuGlyArgHisThrArgGlnMetArgAsnThr......valAl 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTTTTTTATCGGTCTCATGGCCCTGTCCAGTGGGTACCTGGTGGCTTTC 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..PheLeuPheAlaValLeu.....LeuLeuIlePheSer 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGTTACTCCAGAACAAGCATGTTTTCCACAACAATTGCTGTCAGGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nIlePheSerPheValAlaGluPheSerValProLeuLeuIle.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          {\tt aGlySerArgValProGlyArgGlyAlaProIleSerAlaLeuLeuSerI}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATTGTGTCCCATAGCTATGCCACTGTCAGCTCTTTTGTGTTTATTTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CysCysGln 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA; 1841 BP
   Location/Qualifiers
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alignment_block:
US-09-510-332-1 x V53631
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coveil human 7-transmembrane G-protein coupled receptor. HNFDY20
coupling to the coupled served from the coupled receptor. HNFDY20
coupling the coupled served from coupled receptor. HNFDY20
coupling the coupling the coupling the coupling the coupling to the coupling to the coupling the coupling the coupling the coupling to the coupling the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         under expression of the protein. The invention also relates to methods of identifying agonists and antagonists and for using such compounds to treat conditions associated with HNFDY20 imbalance. Diagnostic assays for detecting diseases associated with inappropriate HNFDY20 activity or levels are also provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1841 BP;
                                                                           43
                                                                                                                                                                  26 eIleValValValAsnGlyIleAspLeuIleLysH1sArgLysMetAlaP 43
                                                                                                                                                                                                                                                                                10 PheLeuLeuAlaValIleGlnPheLeuLeuGlyIlePheThrAsnGlyIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 2-4; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides and polypeptides encoding a novel human 7-transmembrane receptor - useful for diagnosing and treating e.g. cancer, osteoporosis and Parkinson's disease and infections caused by HIV-1 or -2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-482962/42.
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           ..GTGGACGTGCTCCTGCTCAACCTGACCGCCTCGGACCTGCTCCTGCTG 484
                                                            roLeuAspLeuLeuSerCysLeuAlaValSerArgIlePheLeuGln 59
                                                                                                                    GCTGGCCCTGGTGGTCTTCGTGGGCAAGCTGCAGCGCCGCCCGGTGGCC.
                                                                                                                                                                                                                            TTCTCGGTGTACCTTCTCACTTTCCTGGTGGGGCTCCCCCCTCAAC...CT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                538 C; 593 G; 376 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 296
Gaps: 18
Percent Identity: 23.986
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                                                                                                                       436
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WXEXEXEX B
                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                  seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1993.DAT:Q43543
                                                                                                                                                                                                                                                     1086 CCCTGAACTCCTGTGTCGACCCCTTTGTCTACTACTTC 1123
Human; rhodopsin; mutant; retinal degeneration; primer; probe
                                              Rhodopsin gene.
                                                                                     11-NOV-1993
                                                                                                                            Q43543;
                                                                                                                                                             Q43543 standard; cDNA; 3129
                                                                                                                                                                                                                                                                                         249 erLeuLysPheHisIleArgArgPheIlePheLeuPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       720 CTGCTCACTGCAGCGTGGTCTACGTCATAGAATTCTCAGGGGACATCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 ly......SerLeuLeuTyrValSerMetIleCys.....ValPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  626 CGCTTCCTGAGTGTGGCCCACCCCCTG.....TGGTACAAGACCCGGCC 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 LysValAlaSerValArgHisProLeuPheIleTrpLeuLysMetArg..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89 snGluLeuGluLeuTrpLeuAlaThrTrpLeuGlyValPheTyrCysAla 105
                                                                                                                                                                                                                                                                                                                                  TATCTGCGGTGAAAGCCCGGCGTGGAGGATCTACGTGACGCTTCTCAGCA 1085
                                                                                                                                                                                                                                                                                                                                                                                                            AACTTCCTTGTCTGCTTTGGGCCCTACAACGTGTCCCATGTCGTGGGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                               SerPheLeuIleLeuTyr.....PheSerHis.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alProGlyArgGlyAlaProIleSerAlaLeuLeu.....SerIleLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGGGGCAGCCACCGCCGGCAGAGGAGG..........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuLeuIlePheLeuPheAlaValLeuLeuIlePheSerLeuGlyAr 203
                                                                                                                                                                                                                                                                                                                                                                       ....Cys.....MetIleLysValPheLeuSerS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9......HlsThrArgGlnMetArgAsnThrValAlaGlySerArgV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGATCATCACCAGCTACTGCTACAGCCGCCTGGTGTGGATCCTCGGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eSerGlnAsnAlaThrIleGln.....LysGluAspThrLeuAlaI 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCACCATCTATCTC...ACCGCCCTCTTCCTGGCAGCTGTGAGCATTGAA 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eIleGluPheIleMetCysSerAlaAsnCysAlaIleLeuLeuPheIleA 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGTTCCTGCCTTTCCGCATGGTGGAGGCAGCCAATGGCATGCACTGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....IleSerLysLeuValProTrpMetIleLeuG
                                                                                 (first entry)
                                                                                                                                                               ВP
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SOXX CCCCCCXX PRANCE AND AXX PRANCE FIRST XXX PRANCE FOR THE FIRST XXX 
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    Quality:
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Percent Similarity:
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US-09-510-332-1 x Q43543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: Q43543 from: 1 to: 3129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence given represents the human rhodopsin cDNA. Mutant versions of this sequence encode proteins which cause retinal degeneration. These sequences may be identified using primers/ probes described in the invention (see also Q43545-48) and may be used to diagnose hereditary retinal degeneration. This sequence is the closest approximation to the gene sequence as the sequence given in the specification is not printed clearly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe or primer contg. sequence of human retinal degeneration slow protein mutant - used to diagnose hereditary retinal degenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Berson EL, Dryja TP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-DEC-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3129 BP; 694 A; 999 C; 654 G; 735 T; 47 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   450 CCCCATCAACTTCCTCACGCTCTACGTCACCGTC......483
                                                                                                                                                                                                                                                                                                                                  484 .....CAGCACAAGAAGCTGCGCACCCCTCTCAACTACATCCTGCTC 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               409
                                                            576 CCTCTACACCTCTCTGCATGGATACTTCGTCTTCGGGCCCACAGGATGCA 625
                                                                                                                                                                                              526 AACCTAGCCGTGGCTGACCTCTTCATGGTCCTAGGTGGCTTCACCAGCAC 575
                                                                                                                                                                                                                                                                                                                                                                          34 spLeuIleLysHisArgLysMet...AlaProLeuAspLeuLeuLeuSer 49
:::|||::::|||:::::::|||||::::::|||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17
                                                                                                                                                                                                                                            50 CysLeuAlaValSerArgIlePheLeuGlnLeuPheIlePheTyrValAs 66
                                                                                                                                    66
83 laIleLeuLeuPheIle......AsnGluLeuGluLeuTrp...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetLeuGluSerHisLeuIleIleTyrPheLeuLeuAlaVallleGlnPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGCTGGCCGCCTACATG......TTCTGCTGATCGTCCTGGGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eLeuLeuGlyIlePheThrAsnGlyIleIleValValValAsnGlyIleA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1993-214088/26.
DB; R38483.
                                                                                                                             nValIleValIlePhePheIleGluPheIleMetCysSerAlaAsnCysA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92WO-US10536
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295..1341
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0.756
49.541
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Gaps: 16
Percent Identity: 21.101
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626 ATTTGGAI 95 676 TTGGTGGI 108 aSerVal :::: 726 CAACTTC 117 rp 147 rAlaGly 147 rAlaGly 1828 C 159 hephese :::::: 907 ATCTACA 176 ILehhes
#ARGGCTTCTTTGCCACCCTG  LeuAlaThrTrpLeuGl
PLEUGLYVALPHETYCCYSALALYSVALAL  PLEUGLYVALPHETYCCYSALALYSVALAL  GCGGTACGTGGTGGTAAAATTGCCCTGTGGTCC  Hisprole  Hisprole  ACCATGCCATCATGGGCGTTGCTTCACCT  ACCATGCCATCATGGGCGTTGCCTTCACCT  ACCATGCCATCATGGGCGTTGCCTTCACCT  ACCATGCCCATCATGGGCGTTGCCTTCACCT  ACCATGCCCCCCACTCGCCGGCTGG  Ill:::::   GCGGACCCCCCACTCGCCGGCTGG  TCCAGGTA  TCCAGGTA  TCCAGGTA  TCCAGGTA  TCTTTTGTC  TIEGLILYSGLUASPTHTLEUALIATIGGIN  TIEST LEUGLYASGLUASPTHTLEUALIATIGGIN  TIEST LEUGLYASGLUASPTHTLATGGINMETA  TIEST LEUGLYATGHISTHTATGGINMETA  TCTTTTTTTTTT  PHESET LEUGLYATGHISTHTATGGINMETA  TCTTTTCACCGTCAAAGAGGCCGCTGCCCAACAGG  TCTTTCACCGTCAAAGAGGCCGCTGCCCAACAGG  TTCACCGTCAAAGAGGCCGCTGCCCAACAGG  TTCACCGTCAAAGAGAGAGNNNGTCACCCGCCATG  TATGVALPTOGLYATGGLYATGGLYATGGLYATGGLACACGCCATGCTTTTT  TATGVALPTOGLYATGGLYATGGLYATGGLACCCCGCATGCTTCCTGCTGGGTNCCCTACGCCCAGGCTTCCCCAACAGG  TTCACCCACCAGGGCTCCAACTTCGGTCCCAACCGCCATGCTTTTTCCTGAAGGCAAGGCAAGGAAGNNNGTCACCCTTCCGCAACGCCCATGCTTCCGCAACGCCCATGCTTCCCGCAACGCCCATGCTTCCCAACCTTCCGCCAACAGGCCAACAGGCCAACAGGCCAACCATGCTTCCAACCTTCCAACCCTTCCAACCTCCAACCATGCTTCCAACACCCTTCTTTTGCCAAAGGCCAACCTCCAACCTCCAACACACGCCTACCACACGCCAACACAGGCCAACAGGCCCAACCAGGCCCACCA

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alignment_scores:
Quality:
Ratio:
Percent Similarity:
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US-09-510-332-1 x V31718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: V31718 from:
470 GTGAGGTACCTCCTGGTGGCATATTCTACGCGTTCCTGGCCCAAG....
                             110 ValArgHisProLeuPheIle.....TrpLeuLysMetAr 121
                                                       420 ACTATTTATATGTCTACTTGGATATCTTCAGTGTTGTGTGCGTCAGTCTA
                                                                                                               382
                                                                                                                                                                   338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence is that of ORF74 of Kaposi's sarcoma herpesvirus (KSHV) which encodes a G protein-coupled receptor. It can be used in the diagnosis and treatment of KHSV infection.
                                                                                                                                                                                                                288 CGATAGATATACTGCTCCTGGGTATCTGCCTAAACTCGCTGTGTCTTAGC
                                                                                                                                                                                                                                                                   250 CACCTACATT.....TTTTGCAAGCACCGATCGCGGGCAGGAG
                                                                                                                                                                                                                                                                                                                    203 ATACTCTCTGATT...TTCCTCATAAATGTTCTTGGAAATGGATTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated Kaposi's sarcoma-associated herpesvirus proteins - comprising antigenic membrane protein, G protein coupled receptor and cyclin protein used to develop products for diagnosis and
                                                                                                                                                                                                                               11 LeuLeuAlaValIleGlnPheLeuLeuGlyIlePheThrAsnGlyIleIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1202 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 50-51; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; W37976.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORR )
                                                                                                          ATATCTCTA....TTGGCAGAAGTGTTGATGTTTTTGTTTCCCCAATAT
                                                                                euTrpLeuAlaThrTrpLeuGlyValPheTyrCysAlaLysValAlaSer 109
                                                                                                                                    eMetCysSerAlaAsnCysAlaIleLeuLeuPheIleAsnGluLeuGluL 93
                                                                                                                                                                                        LeuPheIlePheTyrValAsnValIleValIlePhePheIleGluPheIl 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sarcoma herpesvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Knowles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96US-0728603
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0.867
52.852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= G protein-coupled receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258 A; 279 C; 311 G; 354 T; 0 other;
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Kaposi's sarcoma-associated herpes virus nucleic acid - di:hydro:folate reductase and is useful for treatment, por diagnosis of Kaposi's sarcoma
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                                                                                                     Bohenzky RA,
                                                                                                                                    (UYCO ) UNIV COLUMBIA NEW YORK
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eGlnLysGluAsp...ThrLeuAlaIleGlnIlePheSerPheValAlaG 182
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AC V19941;
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XX KSHV long unique cod:
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KSHV: HHV8; human he:
KW KSHV: HHV8; human he:
KW interleukin-6; IL-6;
KW complement-binding p.
KW immediate early prot.
KW lymphoproliferative '
KW lymphoproliferative '
KW HIV immune status; a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACCACGTACTAAATCTACTGGACACTCTGCTAAGGCGA 24907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                /product= macrophage inflammatory protein complement (27137..27424)
                                                                                                                                                                                                                                                                                                                                                                                            complement (21548..21832)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= glycoprotein B
complement (17261..17875)
                                   89600..90541
                                                                                                                                                   /product glycoprotein M complement (69412..69915)
                                                                                                                                                                                                         /product= protein T1.1 complement (58976..60175)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product complement-binding protein
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                                                                                             glycoprotein L
t (88410..88910)
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interferon regulatory factor
                                                          interferon regulatory
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This sequence represents the long unique region and terminal repeat of the Kaposi's sarcoma-associated herpes virus (KSHY). KSHY is also known as human herpes virus 8 (HHY8). This sequence contains the DNAs of the cinvention which encode KSHV polypeptides selected from: (a) viral fire protein the protein (MIP) II; (b) viral interleukin-6 (II-6); (c) viral IRF 1; (d) complement-binding protein; glycoproteins B, M or I; (d) capsid protein IV encoded by ORF65; and (e) immediate early protein encoded by ORF73. Labelled probes for the nucleic acid, proteins encoded by it, and antibodies (Ab) specific for the proteins are useful for CC detecting HHV8, specifically proteins of Kaposi's sarcoma, in body fluids or tissue samples. HHV8 infections can be treated with antisense created valid and protein can be used in proteins or treated with antisense contain. Ab may be used for prophylaxis or treated with antisense containing the content of the protein can be used in protective vaccines. Ab may also be used the protein can be used in protective vaccines. Ab may also be used cother lymphoproliferative diseases such as lymphomas, leukaemia, containing the concleic acid are useful for drug screening. HHV8-derived peptides can be inhibited with methotrexate. These can also be used to determine the immune status of a batient infected with HTV. HHV8 derived containing the containing the containing the summan status of a batient infected with HTV. HHV8 derived rection and the many of the immune status of a batient infected with HTV. HHV8 derived rection in the containing the containing the containing the summan status of a batient infected with HTV.
  Sequence 137507 BP; 32579 A; 37795 C;
                                                  the immune status of a patient infected with HIV. HHV8 derived protein viral MIP III may be used as an anti-inflammatory agent for, e.g. treating rheumatoid arthritis. This sequence is stated as containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding Kaposi's sarcoma associated herpes proteins - useful for, e.g. detecting levels of HHV8 in, and preparation of vaccines for treatment of, HIV patients
                                           81 open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 135-203; 230pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bohenzky RA,
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25-JUL-1996;
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96US-0687253.
96US-0688814.
96US-0708678.
96US-0728323.
96US-0747887.
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96US-0686349.
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35758 G;
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alignment\_scores:

Quality: Ratio:

Length: Gaps:

263 14

31375

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0 other;

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seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1997.DAT:T79064
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US-09-510-332-1 x V19941
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                                                                                                                                                                                                                                                                                                                                                          130061 TATGCTCTCACCTGGTGTGTGGTGAGGAGGACAAAGCTGCAAGCCAGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129612 CGATAGATATACTGCTCCTGGGTATCTGCCTAAACTCGCTGTGTCTTAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 eValValAsnGlyIleAspLeuIleLysHi8ArgLysMetAla...P
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                                                   TACCACGTACTAAATCTACTGGACACTCTGCTAAGGCGA 130207
                                                                                                  LysValPheLeuSerSerLeuLysPheHisIleArgArg
                                                                                                                                                                                                    euLeuSerIleLeuSerPheLeuIleLeuTyrPheSerHisCysMetIle 243
                                                                                                                                                                                                                                                                                                         nThrValAlaGlySerArgValProGlyArgGlyAlaProIleSerAlaL
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                                                                                                                                                     .....GTGATTGTTGCTGTGGTGCTGCTGTTTTTTGTGTTTTTGCTTCCCT 130168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gIleSerLysLeuValProTrpMetIleLeuGlySerLeuLeuTyrValS 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ....AAGCAGTCCCTCGGATGGGTACTGACATCCGCTGCACTGTTAATTG 12988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    euTrpLeuAlaThrTrpLeuGlyValPheTyrCysAlaLysValAlaSer 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....CCGGTCAGCAAGCAGGCCATGTGTTATGAGAACGCGGGAAA 129975
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alignment_block:
US-09-510-332-1 x T79064
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Percent Similarity:
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T79064 standard; cDNA to mRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Allele; Xenopus laevis; melatonin; receptor; untranslated region; PCR; mRNA; half-life; skin; amplification; primer; polymerase chain reaction; transmembrane domain; cellular signalling; inhibition; adenylyl cyclase; modulation; intracellular; cyclic GMP; inhibitor; phosphodiesterase; ss.
                                                                                                                                                                                                                                                               Sequences T79063-66 represent novel allelic genes of the Xenopus laevis melatonin receptor MEL-IA. The sequences encode proteins which are 65 amino acids shorter than those described in the prior art. Also the last 2 C-terminal amino acids encoded by these sequences are different from the previously known proteins. This sequence is a short form of the novel receptor MEL-IAa also known as Mel 1-c(alpha). As compared to the long form (T79063), the difference occurs in the 3' untranslated region (both sequences encode the same protein), which is thought to affect the half-life of the mRNA. The nucleotide sequence was isolated from CDNA derived from Xenopus skin RNA and amplified using the primers T79067-76. The nucleotide sequence was isolated from control inhibit adenylyl cyclase, but both protein MEL-IAA has been shown to inhibit adenylyl cyclase, but both proteins can modulate intracellular scape.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding functional melatonin receptor of Xenopus for screening for potential (ant)agonists useful for e.g. treating cardiovascular disease and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 28-29; 62pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jockers R, Marullo S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ADIR ) ADIR & CIE.
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                                                                                                                                                                                                                       Sequence 1147 BP; 317 A;
                                                                                                                                                                                                                                                      phosphodiesterase.
2 LeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIleGlnPheLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1997-132635/12
                                                                                                                                                         Quality:
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0.752
53.401
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                                                                                                                                                           rIleLeuSerPheLeuIleLeuTyrPheSerHisCysMetIleLysValP 246
                                                                                                                                                                                                                                                                                    TIGTACTTTTGCAGTTTGCTGGGCCCCCTTAAACTTTATCGGCCTTGCT 795
                                                                                                                                                                                                                                                                                                                    AAAGTTGACACAAACAGACTTGAGAAATTTCTTGACCATGTTTGTGGTCT
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                                            TATATGGTGTGCTAAATCAAAACTTCCGCAAG
                                                                                heLeuSerSerLeuLysPheHisIleArgArg
                                                                                                                           TGTTTTAAGCTATTTCATGGCCTATTTTAACAGTTGTCTCAATGCTGTTA
                                                                                                                                                                                                     GTGGCCATTAATCCGTTTCATGTGGCACCAAAGATTCCAGAATGGCTGTT
                                                                                                                                                                                                                                         val......proGlyArgGlyAlaPro...IleSerAlaLeuLeuSe
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  /cgn2_2/gcgdata/geneseq/geneseqn/NA1997.DAT:T79066
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US-09-510-332-1 x T79066
                                                                                                                                                                                                                                                                                                                Sequences T79063-66 represent novel allelic genes of the Xenopus laevis melatonin receptor MEL-1A. The sequences encode proteins which are 65 melatonin receptor MEL-1A. The sequences encode proteins which are 65 mino acids shorter than those described in the prior art. This sequence is a short form of the novel receptor MEL-1Ab also known as compared to the short form (T79066), the difference cocurs in the 3' untranslated region (both sequences encode the same protein), which is thought to affect the half-life of the mRNA. The protein), which is thought to affect the half-life of the mRNA. The correction, which is thought to affect the half-life of the mRNA. The correction acids. The nucleotide sequence was isolated from CDNA derived from Xenopus skin RNA and amplified using the primers T79067-76. The nucleotide sequence encodes a protein which is a 7 transmembrane receptor involved in cellular signalling. MEL-lab has been shown to modulate the inhibitor of phosphodiesterase, but unlike MEL-laa (T79063) cannot inhibitor of phosphodiesterase, but unlike MEL-laa (T79063) cannot
                                                                      Align seg 1/1 to: T79066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding functional melatonin receptor of Xenopus for screening for potential (ant)agonists useful for e.g. treating cardiovascular disease and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Allele; Xenopus laevis; melatonin; receptor; untranslated region; PCR; mRNA; half-life; skin; amplification; primer; polymerase chain reaction; transmembrane domain; cellular signalling; inhibition; adenylyl cyclase; modulation; intracellular; cyclic GMP; inhibitor; phosphodiesterase; ss.
                                                                                                                                                                                                                                                                          Sequence 1147 BP; 313 A;
                                                                                                                                                                                                                                                                                                          inhibit adenylyl cyclase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 33-34; 62pp; French.
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                              2 LeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIleGlnPheLe
CTCACCTCTGCCCTGGCGGTGGTTCTTATATTCACCATTGTTGTGGATGT 140
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/product= melatonin receptor MEL-lab
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Gaps:
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246 heLeuSerSerLeuLysPheHisIleArgArg 256
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  TCTACGGTCTGCTAAATCAAAACTTCCGCAAG
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                                                                                                                                                                                                                                                                                                                                     AAAGTTGACACCAACAGACTTGAGAAATTTCTTGACCATGTTTGTGGTCT
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seq\_documentation\_block:
ID T79063 standard; cD

cDNA to

mRNA; 1311

/cgn2\_2/gcgdata/geneseq/geneseqn/NA1997.DAT:T79063

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alignment_block:
US-09-510-332-1 x T79063
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                                                                Align seg 1/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus melatonin receptor MEL-1Aa long form coding sequence
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                                                                                                                                                                                                                                                                                                  melatonin receptor MEL-1A. The sequences encode proteins which are 65 amino acids shorter than those described in the prior art. Also the last 2 C-terminal amino acids encoded by these sequences are different from the previously known proteins. This sequence is a long form of the novel receptor MEL-1Aa also known as Mel 1-c(alpha). As compared to the short form (179064), the difference occurs in the 3' untranslated region (both sequences encode the same protein), which is thought to affect the sequences encode the same protein), which is thought to affect the half-life of the mRNA. The nucleotide sequence was isolated from cDNA derived from Xenopus skin RNA and amplified using the primers T79067-76. The nucleotide sequence encodes a protein which is a 7 transmembrane receptor involved in cellular signalling. MEL-1Aa has been shown to inhibit adenylyl cyclase, but both proteins can modulate intracellular newshorked in cellular signalling. MEL-1Aa has been shown to inhibit adenylyl cyclase, but both proteins can modulate intracellular newshorked interests.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding functional melatonin receptor of Xenopus for screening for potential (ant)agonists useful for e.g. treating cardiovascular disease and cancer
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P-PSDB; W25926.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ADIR ) ADIR & CIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequences T79063-66 represent novel allelic genes of the Xenopus laevis
                                                                                                                                                                                                                                                          Sequence 1311 BP; 369 A;
                                                                                                                                                                                                                                                                                         phosphodiesterase.
 91
CTCACCTCTGCCCTGGCGGTGGTTCTTATATTCACCATTGTTGTGGATGT 140
                              LeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIleGlnPheLe 18
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/product= MEL-1Aa receptor protein
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0.752
53.401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATAGCTATTTTCCAGAATGGGTGGACGCTTGGAAATATCCATTGTCAGA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lileValilePhePheIleGluPheIleMetCysSerAlaAsnCysAlaI 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCAG.....ACAGTGAGTTCCTCATACACCATAACAGTAGTGGTGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rGlnAsnAlaThrIleGlnLysGluAspThrLeuAlaIleGlnIlePheS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TyrAlaGlyPheMetVal.....ProTyrPheLeuArgLysPhePheSe 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCTTGGCCTGACATGGATACTAACTATAATTGCAATCGTGCCAAACTTT
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                                                                           heLeuSerSerLeuLysPheHisIleArgArg 256
                                                                                                                    TGTTTTAAGCTATTTCATGGCCTATTTTAACAGTTGTCTCAATGCTGTTA 895
                                                                                                                                                         rIleLeuSerPheLeuIleLeuTyrPheSerHisCysMetIleLysValP 246
                                                                                                                                                                                                GTGGCCATTAATCCGTTTCATGTGGCACCAAAGATTCCAGAATGGCTGTT 845
                                                                                                                                                                                                                                   val......proGlyArgGlyAlaPro...IleSerAlaLeuLeuSe 229
                                                                                                                                                                                                                                                                            TTGTACTTTTTGCAGTTTGCTGGGCCCCCTTAAACTTTATCGGCCTTGCT
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                                                                                                                                                                                                                                                                                                                                                                                           .....MetArgAsnThrValAla.....
                                           TATATGGTGTGCTAAATCAAAACTTCCGCAAG
/cgn2_2/gcgdata/geneseq/geneseqn/NA1997.DAT:T79065
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T79065 standard; cDNA to mRNA;

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alignment_block:
US-09-510-332-1 x T79065
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Quality:
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                                                                                                                                                                   Align seg 1/1 to: T79065
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P-PSDB; W25927.
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                                                                                                           2 LeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIleGlnPheLe 18
        uLeuGlyIlePheThrAsnGlyIleIleValValValAsnGlyIleAspL 35
                                                          CTCACCTCTGCCCTGGCGGTGGTTCTTATATTCACCATTGTTGTGGATGT 140
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1..1065
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/product= melatonin receptor MEL-1Ab
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  271 C;
                                                                                                                                                                                                                                                                                         Length: 294
Gaps: 12
Percent Identity: 19.388
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                                                                                                                                                                                                                                                                                                                                                                                                                                            409 T; 0 other;
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gArg 256  :::	heLeuSerSerLe :: : :   TCTACGGTCTGC	246 896
heLeuIleLeuTyrPheSerHisCysMetIleLysValf :::::::      ::    ::    :: ATTTCATGGCCTATTTTAACAGCTGTCTCAATGCTGTCA	rIleLeuSerPh :::     :: TGTGTTAAGCTA	229 846
ProGlyArgGlyAlaProIleSerAlaLeuLeu 	Val	217 796
CGTTTGCTGGGCACCCTTGAATTTTATCGGC	TGTACTTTTT	746
		214
MetargAsnThrValAla	AAAGTTGACACC	208 696
lePheSerLeuGlyArgHisThrArgGln 	LeuLeuLeuIle :::   ::: TGGGTTTTAGTG	195 646
LuPheSerValProLeuLeuIlePheLeuPheAlaVa. :::       :::       TCTTAGTGTTGTGACATTCTGCTACTTAAGAAT;	erPheValAlaGLuPheSerV    ::::::::::::::     ATTTTATAGTCCCTCTTAGTG	599 8/T
laThrIleGlnLysGluAspThrLeuAlaIleGlnIlePheS    ::::::::::   :::::::::::::::::::::	rGlnAsnAlaTh :       GCAGAC	161 555
lyPheMetValProTyrPheLeuArgLysPhePheS    :::       :::::          :::	TyrAlaGlyPhe ::::::    TTTGTTGGATCA	147 505
llySerLeuLeuTyrValSerMetIleCysValPheHisSerLys    	leLeuGlySerL        ACCTTGGCCTGA	130 455
glleSerLysLeuValProTrpmet   :::       anangacaagctttttaatcaaagaagcacctggttc	<pre>pLeuLysMetArgIleSerLys :::::    :::    CCACAGCCTGAGATATGACAAG</pre>	117 405
ValPheTyrCysAlaLysValAlaSerValArgHisProLeuPheIle 		101 355
LeuLeuPheIleAsnGluLeuGluLeuTrpLeuAlaThrTrpLeuG 	TC le	84 320
IlePhePheIleGluPheIleMetCysSeralaAsnCysAl        	lileval :   ::: CATAGCT	67 270
euAlaValSerArgIlePheLeuGlnLeuPheIlePheTyrValAsnVa    ::::::::::::::::::::::::::::::::::	H — F	51 220
ArgLysMetAlaProLeuAspLeuLeuLeuSer :::   ::: AAGAAGCTGCAGAATGCTGGAAATCTCTTTGTTGTC	euIleLysHis :::::::::: TCCTGAGGAAC	35 170
:::   :::: AATATATTGGTCATTTTG	:         CCTGGGC	141

896

846 246

Sequence

5, Appli 5, Appli 5, Appli 61, Appli 61, Appli 61, Appli 61, Appli 61, Appli 6, Appli 6, Appli 6, Appli 6, Appli

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Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                   pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 length: 0
length: 2000000000
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-510-332-1
1521
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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        US-08-118-270-56
PCT-US93-08528-56
US-08-390-000A-8
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US-08-748-506-22
US-08-748-506-23
US-08-728-603-17
US-08-748-506-24
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US-08-118-270-65
PCT-US93-08528-65
US-08-148-209A-4
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US-08-148-209A-4
US-08-18-270-44
PCT-US93-08528-68
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82.577 Million cell updates/sec
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Sequence 8, Appli
Sequence 8, Appli
Sequence 2, Appli
Sequence 23, Appli
Sequence 17, Appli
Sequence 18, Appli
Sequence 18, Appli
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 65, Appli
Sequence 65, Appli
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51, Appl
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                                                                                 STRANDEDWESS:
TOPOLOGY: line
MOLECULE TYPE: p
US-08-118-270-56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence
   Q
                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION NUMBER: US 07/943,236
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: TOWNSEND, KEVIN G.
NAME: TOWNSEND, KEVIN G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MUTPHY, Randall B.
APPLICANT: Schuster, David I.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G.
TITLE OF INVENTION: RECEPTORS, AND COL
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., SI
                           Query Match
Best Local Similarity
Matches 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                    TELEX: 248633
INFORMATION FOR SEQ ID NO:
                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 419 Seven CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
   1 MLESHLIIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKM-APLDLLLSCLAVSRIFLQ 59
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5. 5508384
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                          8.1%;
ilarity 21.1%;
Conservative 64
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linear
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US-08-476-976-5
US-08-476-976-5
US-08-476-000-61
US-08-472-840-61
US-08-474-410-61
US-08-474-410-61
US-08-076-093A-6
US-08-076-093A-6
US-08-08-20-265-6
US-08-801-238-6
US-08-801-238-6
US-08-801-238-6
US-08-801-238-6
US-08-801-238-6
                           ; Score 123.5; DB 1;
; Pred. No. 4.3e-05;
64; Mismatches 121;
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COMPOSITIONS AND METHODS THEREOF
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                                Indels 73;
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Result No.

Score

123.5 123.5 123.5 122.5 120.5 120.5 110.5 118.5 113.5 113.5 113.5 107 107 104.5 103.5 103.5 103.5 103.5 103.5 103.5 103.5 103.5 103.5

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Title: Perfect score:

Scoring table: Sequence: Run

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                                                 Query Match
Best Local Similarity
                                           Matches
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                                                                                                                                                                                                                              TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                            NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELLERAX: 202-737-3528
                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                          FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                   TOPOLOGY:
                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 QKAEKEVTRMVIIMVIAFLICWVPYASVAFYIFTHQGSNFGPIFMRIPAFFAKSAAIY--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111 GENHAIMGVAFTWV-MALACAAPPIAGW------SRY----IPEGLQCSC 149
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                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington
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419 Seventh Street, N.W., Suite 300
                                      Conservative
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/ENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
/ENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
                                                                                                                                   peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                             single
                                    8.1%; Score 123.5; DB 4;
21.1%; Pred. No. 4.3e-05;
ative 64; Mismatches 121;
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                             73; Gaps
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Matches

Conservative

Length 348; Indels 71;

Gaps

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                   Query Match
Best Local Similarity
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                                                                                                                                                                     TELEFAX: 212 869-8864/
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 69:
                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                             TOPOLOGY: OLFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0
FILING DATE: 17-FEB-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 --KFFSQNATIQKEDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTROMRNTVAGS 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A. ZIP: 10036-2711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 LGGFTSTLYTSLHGYFYFGPTGCNLEGFFATLGGEIALWSLWLAIERYVVVCKPMSNFRF 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New York .
                                                                                                                                                          348 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sealfon,
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                                                                                                        protein
8.1%; Score 123.5; DB 2;
20.8%; Pred. No. 4.9e-05;
ative 63; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stuart C.
Cloning and Expression of
Gonadotropin-Releasing Hormone Receptor
                                                                                                                                                                                                                                                                                                                                                                                                              Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                US/08/390,000A
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                                                                                                                                                                                                                                                                                                                                                                                                              Version #1.25
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                                                                  ; MOLECULE TYPE: US-08-820-521-2
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: CDNA CLONE HNFDY20 THAT ENCODES TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 RVPGRGAPISALLSILSFLILYESHCMIKVFLSSLKFHIRRFIFL----FFILVIGIYPS 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 GIDYYTLKPEVNNE---SFVIYMFVVHFTIPMIIIFFCYGQLVFTVKEAAAQQQES-ATT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 FGENHAIMGVAFTWVMALACAAPPLAGW------SRY----IPEGLQCSC 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 ----HPL----FIW---LKMRISKLVPWMILGSLLYVSMICVFHSKYAGFMVPYFLR--- 157
                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272 GHSLILILGNPKLKQNAKKFLLHSKCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/820,521 FILING DATE: 19-MAR-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 709 Swederand CITY: King of Prussia
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                                                                                                                        STRANDEDNESS:
                                                                                                         TOPOLOGY:
                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                               TELEFAX: 610-270-4026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QKAEKEVTRMVIIMVIAFLICWVPYASVAFYIFTHQGSNFGPIFMTIPAFFAKSAAIY--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --KFFSQNATIQKEDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGS 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -NPVIYIMMNKQF----RNCMLTTICC 323
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Fuetterer, Wendy
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                                                                                                           linear
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   8.1%;
24.0%;
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   Score 122.5; DB 2; Pred. No. 7.3e-05;
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                        Length 401;
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                                                                       Matches
                                                                                                                                                                                                                                                                           TELEFAX: 312-616-5700 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NOVEL SPERM RECEPTORS NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 TLAI----QIFSFVAEFSVPLLIFLFAVLLLIFSLGR---HTROMRNTVAGSRVPGRGAP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 QAGLVSVACWLLASAHCSVVYVIEFSGDISHSQ------GTNGTCYLEFRKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 ---ISKLVPWMILG---SLLYVSMIC--VFHSKYAGFMVPYFLRKFFSQNATIQ---KED 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 ANGMHWPLPFILCPLSG--FIFFTTIYL-TALFLAAVSIERFLSVAHPL--WYKTRPRLG 185
                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 327 amino acids
                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   278 VAGILAATILNFLVCFGPYNVSHVVGYICGESPAWRIYVTLLSTLNSCVDPFVYYF 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 QLAILLPVRLEMAVVLFVVPLIITSYCYSRLVWILGRGGSHRRQRR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 ISALL--SILSFLILY----FSH-----C-----MIKVFLSSLKFHIRRFIFLF 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 FLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQLFIFYVNVIV 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 08-NOV CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 6 FILING DATE: 09-NOV-1995
                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
 28
                                                                   7.9%; Score 120.5; DB 3;
Local Similarity 23.4%; Pred. No. 9.2e-05;
Les 64; Conservative 48; Mismatches 110;
                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                5 HL-IIYELLAVIQELLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLS-----CLAVSRIF 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLRILFFLLHLLAYLASLMGNMLIITITCVD---HRLQTPMYFFLSMFSSVECCFITTVI 84
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                                                                                                                                                                                                                   amino acid
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                                                                                                                                                                                      Matches
                                                                                                                                                                                                                     Query Match
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 312-616-5700 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSE: 1-2-2-1-
                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 312-616-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 60/033,751
FILING DATE: 09-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NOVE
111 RHPLFIWLKMRISKLVPWMILGSLLYVS-MICVFHSKYAG-FMVPVFLRKFFSQNATIQK 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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Chicago
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                                                                                                                                                                                    Local Similarity 23.4 es 64; Conservative
                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
SOFTWARE: Patenti
                                                                                                                                            5 HL-IIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLS-----CLAVSRIF 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 08-NOV
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                                                                             LQLFIFYVNVIVIF----FIBFIMCSANCAILLFINELELWLATWLGVF----YCAKVASV 110
                                              PQLL----TIILSGRQKIPFMACISQAFVYLVVGATGFFL---LGVLSLDRFLAICKPL 136
                                                                                                              HLRILFFLLHLLAYLASLMGNMLIITITCVD---HRLQTPMYFFLSMFSSVECCFITTVI 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SETRSIEMLFETL----ALIVLFASLLIAIFAYS-----NIVVTIVRLPSARERQRA- 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDTLAIQIFSFVAEFSVPLLIFLFAVLLL-IFSLGRHTRQMRNTVAGSRVPGRGAPISAL 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Application US/08748506
6159707
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                               Score 120.5; DB 3;
Pred. No. 9.2e-05;
8; Mismatches 110;
                                                                                                                                                                                                              DB 3;
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                                                                                                                                                                                                          Matches
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Best Local Similarity 22.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (716)
INFORMATION FOR SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                            125 LVPWMILGSLLYVSMI-----CVFHSKYAGFMVPYFLRKFFSONATIQKED-TLAIQIFS 178
                                                              106 MFLFPNIISTGLCRLEIFF----YYLYVYLDIFSVVCVSLVRYLLVAYSTRSWPK---KQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
159 SLGWYLTSAALLIALYLSGDACRHRSRVVD---PVSKQAMCYENAGNMTADWRLHVRTVS 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES
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                                                                                               70 IFFIEFIMCSANCAILLFINELELWLATWLGVFYCAKVASVRHPLFI-----WLKMRISK 124
                                                                                                                                 53 ILSLI-FLINVLGNGLVTYI----FCKHRSRAGAIDILLLGICLNSLCLSISL--LAEVL
                                                                                                                                                                 11 LLAVIQFLLGIFTNGIIVVVNGIDLIKHRKMA-PLDLLLSCLAVSRIFLQLFIFYVNVIV 69
                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 190,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 22-JAN CLASSIFICATION: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSILSFLILYFSHCMIKVFLSSLKFHIRRFIFL 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Application US/08785928 6087115
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: New York
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Arvanitakis, Leandros
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| Juare, P.O. Box 1051
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                                                                                                                                                                                                   56; Mismatches
                                                                                                                                                                                                                     Score 120.5; DB 3 Pred. No. 9.7e-05;
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                                                                                                                                                                                                                                     DB 3;
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; Sequence 17, Application U
; Patent No. 6093806
; GENERAL INFORMATION:
APPLICANT: Cesarman, F
; APPLICANT: KNOWLES, DE
; APPLICANT: KNOWLES, DE
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US-08-728-603-17
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; MOLECULE TYPE: protein
US-08-728-603-17
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Best Local Similarity
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APPLICATION NUMBER: US/08/728,603
FILING DATE: 10-OCT-196
CLASSIFICATION: 435
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                216 VTAGFLLPL----ALLILFYALTWCVVRRTKLQARRKVRG--
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LENGTH: 342 amino acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                    106 MFLFPNIISTGLCRLEIFF----YYLYVYLDIFSVVCVSLVRYLLVAYSTRSWPK---KQ 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: BRAMAN, SUSAN J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19
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CITY: Rochester
                                                                                                                                               125 LVPWMILGSLLYVSMI-----CVFHSKYAGFMVPYFLRKFFSQNATIQKED-TLAIQIFS 178
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   234 LILYFSHCMIKVFLSSLKFHIRR 256
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                                                                                                                                                                                                                                                                                            11 LLAVIQFLLGIFTNGIIVVVNGIDLIKHRKMA-PLDLLLSCLAVSRIFLQLFIFYVNVIV 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                        FVAEFSVPLLIFLFAVLLLIFSLG----RHTR-QMRNTVAGSRVPGRGAPISALLSILSF 233
                                                                                                             SLGWVLTSAALLIALVLSGDACRHRSRVVD----PVSKQAMCYENAGNMTADWRLHVRTVS 215
                                                                                                                                                                                                                       IFFIEFIMCSANCAILLFINELELWLATWLGVFYCAKVASVRHPLFI-----WLKMRISK 124
                                       VTAGFLLPL----ALLILFYALTWCVVRRTKLQARRKVRG--
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Clinton Square, P.O. Box 1051
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                                                                                                                                                                                                                                                                                                                                     7.9%; Score 120.5; DB 3; 22.4%; Pred. No. 9.7e-05; ative 56; Mismatches 95;
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US-08-928-692-12
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; MOLECULE TYPE:
US-08-928-692-12
US-08-466-103A-2; Sequence 2, App
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Patent No.
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INFORMATION FOR SEQ ID NO: 12:
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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NAME: Lambiris, Elias J
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                                                                                                                                                                                                                                                                                                    304 ILVALMIHVAQQFSGI--NGIFYYSTSIFQTAGIS-----KPVYATIGVGAVNNVFTA 354
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REFERENCE/DOCKET NUMBER: 4944.200-US
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                                                                                                                                                                                                                                                                  60 LFIFYVNVIVIFFIBFIMCSANCAILLFINELELWLATWLGVFYCAKVASVRHPLFIWLK 119
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                                                                                                                                                            LVLLNKFSWM-----SYVSMIAIF--LFVSFFEIGPGPIPWFMVAEFFSQG---PRPAAL 436
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55; Conserv
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Application US/08466103A
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Lamsa, Michael
                                                                                                                                                                                                                                                                                                                                                                          7.8%; Score 118.5; DB 2; Llarity 24.8%; Pred. No. 0.00026; Conservative 30; Mismatches 64;
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/466,103A FILING DATE: 06-JUN-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/319,887 FILING DATE: 07-OCT-1994 PRIOR APPLICATION DATA: APPLICATION UMBER: 08/261,857 FILING DATE: 17-JUN-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 5856124
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INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 420 amino acid
                                                                                                                                                                                                                                             139
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MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
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ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                             256 WAPLNFIGLAVAINPEHVAPKIPEWLEVLSYFMAYFNSCLNAVIYGVLNQNFRK 309
                                                                                                                                                                 197
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                                                                                                                                                                                                                                                                      121 RISKLV----PWMILGSLLYVSMICVFHSKYAGFMV--PYFLRKFFSQNATIQKEDTLAI 174
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APPLICANT: Ebisawa, Takashi
IITLE OF INVENTION: HIGH-AFFINITY MELATONIN
RECEPTORS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                           84
                                                                                                                                                                                                                                                                                                                                               61 FIFYVNVIVIFFIEFIMCSANCAILLFINELELWLATWLGVFYCAKVASVRHPLFIWLKM 120
                                                                                                                                                                                                                                                                                                                                                                                        31 LTSALAVVLIFTIVVDVLG----NILVI----LSVLRNKKLQNAGNLFVVSLSIADLVVAV 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34
REFERENCE/DOCKET NUMBER:
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                                                                                                                -----GSRV----PGRGAP-ISALLSILSFLILYFSHCMIKVFLSSLKFHIRR 256
                                                                                                                                                       VVVHFIVPLSVVTFCYL-RIWVLVIQVKHRVRQDFKQKLTQTDLRNELTMFVVFVLFAVC
                                                                                                                                                                                            QIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQ------MRNTVA------
                                                                                                                                                                                                                                   RYDKLYNQRSTWCYLGLTWILTIIAIVPNFFVGSLQYDPRIFSCTFAQ--TVSSSYTITV 196
                                                                                                                                                                                                                                                                                                             YPYPVILIAIFQNGWTLGNIHCQISGFLMGLSV----IGSVFNITAIAINRYCYICHSL 138
                                                                                                                                                                                                                                                                                                                                                                                                                           LESHLIIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKMAPL-DLLLSCLAVSRIFLQL 60
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RESULT 12
US-08-458-970A-11
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                                                                             Sequence 11, Application US/08458970A Patent No. 5861272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 312-616-5700
INFORMATION FOR SEQ ID NO: 24
SEQUENCE CHARACTERISTICS:
LENGTH: 327 amino acids
TYPE: amino acid
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 7.7%; Score 117.5; DB 3; Length 327; Best Local Similarity 22.1%; Pred. No. 0.00019; Matches 60; Conservative 51; Mismatches 112; Indels 49
                                        GENERAL INFORMATION:
APPLICANT: LI, ET
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOY-1996
CLASSIFICATION: 435
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                       TITLE OF INVENTION: (
  NUMBER OF SEQUENCES:
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ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER:
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APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
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CITY: Chicago
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Two Prudential Plaza, Suite 4900
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C5a Receptor
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12;

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN ADDRESSEE: CECCHI, STEWART & OLSTEIN

STREET:

6 BECKER FARM ROAD

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US-08-118-270-65
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Best Local (
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                                            Sequence 65, Application US/08118270 Patent No. 5508384
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              GENERAL INFORMATION:
APPLICANT: Murphy
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APPLICATION NUMBER: PCT/US94/09234
FILING DATE: 16 AUG 1994
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC
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 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                         114 -----LFIWLKMRISKLVPWMILGSLLYVS----MICVFH-----
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                                                                                                                                                    301 YGFLGKKFKRY-FLQLLKYIPPKAKSHS 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                         82 LWAVYTAMEYRWPFGNYLCKIASASVSFNLYASVFLLTCLSI---DRYLAIVHPMKSRLR 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 IFYVNVIVIFFIEF--IMCSANCAILLFINELELWLATWLGVFYCAKVASVRHP----- 113
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                                                                                                                                                                                                                                                     LLIFLFAVLLLIFSLGRHTROMRNTVAGSRVPGRGAPISALLSILSFLILYFSHCMIKVF 246
                                                                                                                                                                                                                                                                                                                       SKYAGFMVPYF------LRKFFSQNATIQKED----TLAIQIFSFVAEFS-VP 186
                                                                                                                                                                                    LSSLKFHIRRFIFLFFILVIGIYPSGHS 274
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Murphy, Randall
Schuster, David
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Pred. No. 0.00053;
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RESULT 14
PCT-US93-08528-65
; Sequence 65, Application PC/TUS9308528
; GENERAL INFORMATION:
; APPLICANT: New York University

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SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MU
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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CITY: Washington
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                                                                                                                                                          176 IFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGS---RVP---GRGAPISALLS 229
                                                                                                                                                                                             108 VIVSSRIZVLGSW---AGGEGISMVKVFLISRLSYCGPNTINHFFC-----DVSPLL 156
                                                                                                                                                                                                                 MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                             288 AKKFL 292
                                                              208 HLTVVIIFYA---ASIFIYARPKALSAFTDNKLVSVLYAVIVPLFNPIIYCLRNQDVKRA 264
                                                                                           230 ILSFLILYFSHCMIKVFLSSLKFHIRRFI--FLFFILVIGIYPSGHSLILILGNPKLKQN 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 202-737-3528
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 265 LRRTL 269
                                                                                                                                                                                                                                                             48 TIPKLMGFIGSKENHGQLISFFACMTQLYFFLGLGCTECVLLAVMAYDRYVAICHPLHYP 107
                                                                                                                                                                                                                                                                                        68 IVIFFIEFIMCSANCAILL--FINELELWLATWLGVFYCAKVA------SVRHPLF-- 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                         8 IYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQLFIFYVNV 67
                                                                                                                                                                                                                                                                                                                           1 LLFFLSLLXYVLVLTENMLIIIAIRNHPTLHKPM------YFFLFLEIWYVTV
                                                                                                                              NLSCTDMSTAELTDFVIAIFILLGPL-----SVTGASYMRIPSAAGRHKAFSTCAS
                                                                                                                                                                                                                                                                                                                                                                                             66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         419 Seventh Street, N.W., Suite 300
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                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide
                                                                                                                                                                                                                                                                                                                                                                                           7.0%; Score 107; DB 1; Length 286; 21.6%; Pred. No. 0.0019; rative 52; Mismatches 131; Indels
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RESULT 15
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                         Sequence 4, Application US/08148209A Patent No. 5556780
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Best Local Similarity
Matches 66; Conserv
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release
CURRENT APPLICATION DATA;
APPLICATION NUMBER: PCT/US
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA;
APPLICATION NUMBER: US 07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: 11 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                   108
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LENGTH: 286 amino acid
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                                                                                                                                        265 LRRTL 269
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                                                                                                                                                                                                         208 HLTVVIIFYA---ASIFIYARPKALSAFTDNKLVSVLYAVIVPLENPIIYCLRNQDVKRA 264
                                                                                                                                                                                                                                           230 ILSFUILYFSHCMIKVFLSSLKFHIRRFI--FLFFILVIGIYPSGHSLILILGNPKLKQN 287
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                                                                                                                                                                                                                                                                                                                                                                                           116 IWLKMRISKLVPWMILGSLLYVSMICVFHSKYAGFMVPYFLRKFFSQNATIQKEDTLAIQ 175
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 202-628-51
TELEFAX: 202-737-3528
TELEX: 248633
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OPERATING SYSTEM:
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REFERENCE/DOCKET NUMBER: MU
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                                                                                                                                                                                                                                                                                                                                                                                                                                 TIPKLMGFIGSKENHGQLISFFACMTQLYFFLGLGCTECVLLAVMAYDRYVAICHPLHYP 107
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419 Seventh Street, N.W., Suite 300
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US 07/943,236
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TELEX: 910 277299
INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND BETTERM I
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A-58491-1/BIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: TYPE-2 ANGIOTENSIN II RECEPTOR AND GENE
NUMBER OF SEQUENCES: 16
301 FYGFLGKKFKKY-FLQLLKYIPPKAKSHS 328
                                                                                                                                                                                            145 SKYAGFMVPYF------LRKFFSQNATIQKED----TLAIQIFSFVAEFS-VP 186
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                                                                                                                                                                                                                                                                                                                                                   62 IFYVNVIVIFFIEF--IMCSANCAILLFINELELWLATWLGVFYCAKVASVRHP----- 113
                                                                                                                                                                                                                                                                                                                                                                                           24 HSYIFVMIPTLYSIIFVVGIFGNSLVVIVIYF-YMKLKTVASVFLLNLALADLCFLLTLP 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 6.9%;
Local Similarity 21.3%;
hes 70; Conservative 5
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CITY: San Francisco
STATE: California
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ZIP: 94111-4187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                       FLSSLKFHIRRFIFLFFILVIGIYPSGHS 274
                                                                           HQIFTF--LDVLIQLGVIHDCKIAD-IVDTAMP-----
                                                                                                               LLIFLFAVLLLIFSLG-RHTRQMRNTVAGSRVPGRGAPISALLSILSFLILYFSHCMIKV 245
                                                                                                                                                           KNILGELEPELIILTSYTLIWKALKKAYEIQKNKPRNDDIFRIIMAIVLFEE---FSWVP
                                                                                                                                                                                                                                  RTMLVAKVTCIIWLMAGLASL-PAVIHRNVYFIENTNITVCAFHYESRNSTLPIGLGLT 198
                                                                                                                                                                                                                                                                              amino acid
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 104.5; DB 1; Length 359; Pred. No. 0.0044;
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Search completed: March 15, Job time: 4696 sec

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Perfect score:
Sequence:
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                                                                                                                                                                                                                                                            Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2_2/gcgda
2: /cgn2_2/gcgda
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Gapop 10.0 , Gapext 0.5
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cgn2_2/gcgdata/geneseq/geneseqp/AA198 .DAT: *
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/cgn2_2/gcgdata/geneseq/geneseqp/AA1983.DAT:*
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Y42388
R381483
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W02707
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133.124 Million cell updates/sec
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                                                                                                  Amino acid sequenc
Rhodopsin protein.
Rhodopsin. Homo s
G-protein coupled
G-protein coupled
Human 7-transmembr
Kaposi's sarcoma a
                                                                                                                                                                                                                                                                Description
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Rat glucose transp		Human / Transmembr	G-protein coupled	Rhodopsin Protein. Rhodopsin Homo s	Description Amino acid sequenc		ibution.	nce to have a	99. DAT: * 99. DAT: * 999. DAT: *	995.DAT: *	993.DAT: *	991.DAT: * 992.DAT: *	989. DAT: *	37.DAT: *	43. DAT: * 15. DAT: * 15. DAT: *	11.DAT: * (2.DAT: *	0.DAT:*				8485			מתר בנחטתככע בשט	000 00000	ion cell updates/sec	.8 Seconds gnments)			
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(GEMY ) GENI	18-FEB-1998; 17-FEB-1999;	18-FEB-1999;	26-AUG-1999.	W09942470-A1	M1sc-d1fference	Protein	Key Peptide	Homo sapiens.	secreted protein; signal sequence creceptor.	Amino acid sequence of pt127_1.	09-DEC-1999	Y42388;	12388	LT 1		45 102		102 41 102							1	22 108 23 107.5 24 107	109.5		:	3 117.5 4 117.5
GENETICS INST				•	\\ o	21. /lai	Loc: 8 /1al		tein; cl nce clo	equence	(first entry)		standard; Protein;			.7	, ', ', ', '	. 7			ο α	 			00	7.1 7.1 7.0				7.7
ST INC.	98US-0075038. 99US-0251600.	99WO-US03458			/label= Unk /note= "enc	.256 bel= Mat	ation/Qu 20 bel= Lea		ona libr ning; hy	of ptl2	entry)																	476 21 362 20		
		•			Unknown encoded by twa"	Mature protein	Location/Qualifiers 820 /label= Leader/Signal peptide		); cDNA library; clone; transmembrane cloning; hybridization cloning; gene	7_1.			256 AA.		ALIGNMENTS	Y41087	Y41092 Y41086 Y41085	¥41089 ¥77728	Y88442 Y87466	W48731 Y24952	W12243 W12243	W19100 W85047	Y34786 Y79383 W10108	R25834 W21666	W02716 W86323	1/9303 R27875 R48744	119909 119909	Y70157 Y16630	P90554 Y27593	Y13352 Y83225
									ane protein; ene therapy;							Human lectomedin-1	Peptide seg id No: Human lectomedin-1 Human lectomedin-1	Human lectomedin-1 Human G protein-co	G-protein coupled Human APJ receptor	Human R20 seven tr G protein-coupled	Guinea pig platele Seven transmembran	A human 7-transmem	Amino acid sequenc Human G protein co Rat pheromone rece	Guinea pig platele Rat spermatid chem	G-protein coupled Kidney injury asso	Odorant receptor c	B. burgdorferi ant B. burgdorferi ant Human G protein CO	taphylococcus uman Putative	Bovine rhodopsin. Human secreted pro Rhodopsin amino ac	Amino acid sequenc PRO288 Polypeptide

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Best Local Sin
Matches 74;
                                                                                                         R38483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, hematopolesis regulating activity, tissue growth activity, hemostatic and thrombolytic activity, chemotactic/chemokinetic activity, hemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumor invasion suppressor activity, and tumor invasion suppressor activity, and tumor inhibition activity. The PNs are also stated to be useful for gene therapy. Other activities include inhibiting the growth, infection or function of bacteria, fungi, viruses and other parasites; effecting bodily characteristics such as, e.g. weight, color, skin, etc., effecting bodily characteristics such as, e.g. weight, color, skin, etc., effecting browths or caricadic cycles; enhancing fertility, treatment of depression; treatment of pain; hormonal or endocrine activity.
                 hereditary.
                                                    Rhodopsin protein
                                                                               11-NOV-1993
                                                                                                                               R38483 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is the mmino acid sequence of the pt127_1 protein, which is derived from the pt127_1 clone isolated from a human adult blood (lymphoblastic leukemia MOLT-4) cDNA library.

The PNS and proteins of the invention are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jacobs
Treacy
                            Human; rhodopsin;
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                                                                                                                                                                                             kvhikalqtvtsflllf 238
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                                                                                                                                                                                                                                          dpthlsdmtvttlan1-ipftlsllsflllicslckhlkkm-----qfhgkgspdsnt 221
                                                                                                                                                                                                                                                                KEDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTROMRNTVAGSRVPGRGAP----
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                                                                                                                                                                                                                                                                                                                  LKMRISKLVPWMILGSLLYVSMIC------VFHSKYAGFMVPYFLRKFFSQNATIQ 167
                                                                                                                                                                                                                                                                                                                                                                  VIVIFFIEFIMCSANCAILLFI-----NELELWLATWLGVFYCAKVASVRHPLFIW 117
                                                                                                                                                                                                                                                                                                                                                                                       iifsilvvvtfvlgnfangfivlvnsiewvkrqkisfadqiltalavsrvgl-----lw 60
                                                                                                                                                                                                                                                                                                                                          vilxhwyatvlnpgsyslgvrittinawavtnhfsiwvatslsifyllkianfsnfiflh 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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Agostino I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256
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                                                                               (first entry)
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                           mutant; retinal degeneration; primer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.3%; Score 263.5; DB 2 28.8%; Pred. No. 7.9e-23;
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MJ, Steininger
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                           probe;
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                                                             R93116 standard;
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DB; Q43543.
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             (first entry)
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                                                             Protein;
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The sequence given represents the human rhodopsin protein. Mutant rhodopsin proteins cause retinal degeneration. The DNA encoding the mutant DNA sequences may be identified using primers/probes described in the invention (see also 043545-48) and may be used to diagnose
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hereditary retinal degeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 LFIFYVNVIVIFFIEFIMCSANCAILLFI----NELELW----LATWLGVFYCAKVASVR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MLESHLIIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKM-APLDLLLSCLAVSRIFLQ
-npviyimmnkqf----rncmltticc 323
                                                GHSLILILGNPKLKQNAKKFLLHSKCC
                                                                                                 qkaekxvtrmviimviaflicwvpyasvafyifthqgsnfgpifmtipaffaksaaiy--
                                                                                                                                                                                                   gldyytlkpevnne---sfvlymfvvhftlpmiliffcygglvftvkeaaaggges-att
                                                                                                                                                                                                                                                                                                                                                         ----HPL----FIW---LKMRISKLVPWMILGSLLYVSMICVFHSKYAGFMVPYFLR---
                                                                                                                                                                                                                                                    --KFFSQNATIQKEDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGS
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                                                                                                                                                     RVPGRGAPISALLSILSFLILYFSHCMIKVFLSSLKFHIRRFIFL----FFILVIGIYPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.2%; Score 124.5; DB 1
20.8%; Pred. No. 2.1e-06;
tive 63; Mismatches 125
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Rhodopsin

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24-JAN-1990;
11-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                           This sequence represents human rhodopsin, and is encoded by sequences T17115 (without introns) and T17116 (with introns). Substitution of histidine for the normal nonpolar amino acid proline at position 23 results in a dysfunctional or absent molecule, affecting rod function, and is linked with autosomal dominant retinitis pigmentosa. Probes and primers specific for this mutation may be used as diagnostic agents. Mutations in the campendate pigmentosa. Detection slow protein and retinal rod cGMP-phosphodiesterase genes are also implicated in retinitis pigmentosa. Detection of any of these mutations in a foetus or patient may be used in diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diagnosis of hereditary retinal degenerative diseases e.g. retinitis pigmentosa, - caused by a human photoreceptor protein mutation, by detection of the mutation by PCR amplification or hybridisation
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DB; T17115, T17116.
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RVPGRGAPTSALLSILSFLILYFSHCMIKVFLSSLKFHIRRFIFL----FFILVIGIYPS::::::|||::::|||::||
                                          gidyytlkpevnne---sfviymfvvhftipmiiiffcygqlvftvkeaaaqqqes-att
                                                                                                                     ----HPL----FIW---KMRISKLYPWMILGSLLYVSMICVFHSKYAGFMVPYFLR---
                                                                                                   fgenhaimgvaftwvmalacaapplagw------
                                                                                                                                                           lggftstlytslhgyfvfgptgcnlegffatlggeialwslvvlaieryvvvckpmsnfr
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                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                      348
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                                                                                                                                                                                                                                                                                Conservative
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90US-0469215.
91US-0805123.
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                                                                                                                                                                                                                                                                                            8.2%;
                                                                                                                                                                                                                                                                              64;
                                                                                                                                                                                                                                                                                             Score 124.5; DB : Pred. No. 2.1e-06
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RESULT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G-protein coupled receptor; ligand binding as psychotic disorder; schizophrenia; dopamine; muscarinic acetylcholine; adrenergic; endothe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rhodopsin; opsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R48735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murphy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 111-112; 160pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptides of G-coupled receptor proteins (
                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                            Proteins R48685-R48758 represent a range of G-protein coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYNY ) UNIV NEW YORK STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244
   112
                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -npviyimmnkqf----rncmltticcr 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GHSLILILGNPKLKQNAKKFLLHSKCCQ 299
: :| |: |: : | : ||:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1994-101120/12
                                                         LFIFYVNVIVIFFIEFIMCSANCAILLFINEL-----ELWLATWLGVFYCAKVASVR- 111
                                                                                      mlaaym---fllivlgfpinfltlyvtv-----qhkklrtpinyillnlavadlfmv
                                                                                                                  MLESHLIIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKM-APLDLLLSCLAVSRIFLQ
                            lggftstlytslhgyfvfgptgcnlegffatlggeialwslwlaieryvvvckpmsnfrf 110
---HPL----FIWLKMRISKLVP----WMILGSLLYVSMICVFHSKYAGFMVPYFLR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RB,
                                                                                                                                                69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coupled
                                                                                                                                                                                                                      309
                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     odorant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human rhodopsin protein.
                                                                                                                                                             8.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytomegalovirus.
                                                                                                                                                64;
                                                                                                                                                             Score 123.5; DB 1
Pred. No. 2.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   endothelin; bombesin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 assay; transmembrane
e; cAMP; adenosine; tl
                                                                                                                                                                               DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GPRs) -
                                                                                                                                                   Indels
                                                                                                                                                                            Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful
                                                                                                                                                  73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      endocrine;
                                                                                                                                                  Gaps
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     Query Match
Best Local S
Matches 69
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                                                                                                                                                                                                              Proteins W02657-W02730 represent a range of G-protein coupled receptor (GPR) proteins selected from CAMP, adenosine, muscarinic acetylcholine, adrenergic, thrombin, endocthelin, bombesin, endocrine, rhodopsin, opsin, odorant, cytomegaloviral and other GPR proteins. The receptor proteins were used to design polypeptides, pref. based on the transmembrane domains, for use in G-protein coupled receptor ligand binding assays. The polypeptide fragments retain biological activity such as binding a GPR ligand or modulating GPR ligand binding to a GPR (see W02747-W0299) for examples of polypeptide fragments). The polypeptide fragments can be used in compositions for treating subjects suffering from a pathology chickers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        schizophrenia; dopamine; cAMP;
muscarinic acetylcholine; endot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G-protein coupled receptor; ligand binding assay; transmembrane domain; schizophrenia; dopamine; cAMP; adenosine; thrombin; adrenergic; opsin;
                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-208785/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-SEP-1993;
10-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US5508384-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G-protein
                                                                                                                                                                                                   schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYNY ) UNIV NEW YORK STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-SEP-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 odorant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dopamine receptor peptide - useful as antipsychotic agent, e.g. treating schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G
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        69; Conservative
                                                                                                                                                  309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Column 139-140; 184pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schuster
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92US-0943236.
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                            8.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cAMP; adenosine; thrombin; adrene;
endothelin; bombesin; endocrine;
serotonergic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      309
        64;
Score 123.5; DB 17
Pred. No. 2.3e-06;
4; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
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                                                         DB 17;
     Indels
                                                      Length
                                                         309;
  73;
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271
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RESULT
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This polypeptide comprises HNFDY20, a novel human 7-transmembr G-protein coupled receptor that shows about 30.8% identity in amino acid residues with the thrombin receptor. Its amino aci sequence was deduced from an isolated HNFDY20 polypucleotide sequence (see V53631). The invention relates to HNFDY20 polypeptides and recombinant materials and methods for their
                                                                                                                                              New polynucleotides and polypeptides encoding a novel human 7-transmembrane receptor - useful for diagnosing and treations cancer, osteoporosis and Parkinson's disease and infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                             HNFDY20; G-protein coupled receptor; human; infection; HIV; pain; cancer; anorexia; asthma; Parkinson's disease; acute heart failur hypotension; hypertension; urinary retention; osteoporosis; angina pectoris; myocardial infarction; ulcer; allergy; benign prostatic hypertrophy; psychosis; anxiety; schizophrenia; manic depression; delirium; dementia; mental retardation; dyskinesia; Huntingdon's disease; Gilles de la Tourette's syndron
                                                                                                         Claim
                                                                                                                                    by HIV-1 or -2.
                                                                                                                                                                                                                                                    Bergsma
                                                                                                                                                                                                                                                                                                            19-MAR-1997;
                                                                                                                                                                                                                                                                                                                                       16-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                  23-SEP-1998
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                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                             EP866126-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    therapy; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human 7-transmembrane receptor HNFDY20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W59924;
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DB; V53631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gidyytlkpevnne---sfviymfvvhftipliif-fcygqlvftvkeaaaqqqes-att
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genhaimgvaftwv-malacaappiagw-----sry----ipeglqcsc
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                                                                                        (CORR ) CORNELL RES FOUND INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence is that of a G-protein-coupled receptor 6 by ORF74 of Kaposi's sarcoma herpesvirus (KSHV). It caused in the diagnosis and treatment of KHSV infection.
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                                                                                                                                                                                                                                     Sequences W25926-7 represent novel allelic xenopus laevis melatonin receptor MEL-1A proteins. This sequence is a new form of the melatonin receptor designated MEL-1Aa, also known as Mel 1 -c(alpha). The protein differs from previously known receptors by being 65 amino acids shorter and also having 2 different C-terminal amino acids. The protein is encoded by 2 different alleles (T79063-4) which differ in the 3' untranslated region (both sequences encode the same protein), which is thought to affect the half-life of the mRNA. The coding sequence was isolated from cDNA derived from Xenopus skin RNA and amplified using the primers T79067-76. The nucleotide sequence encodes a 7 transmembrane receptor involved in cellular signaling. MEL-1Aa has been shown to CGMP, esp. inhibiting its accumulation induced by an inhibitor of phosphodiesterase.
                                                                                                                                                                                                                               cGMP, esp. inhibit phosphodiesterase.
                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Page 25-26; 62pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding functional melatonin receptor of Xenopus for screening for potential (ant)agonists useful for e.g. treating cardiovascular disease and cancer
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      139
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                    RISKLV----PWMILGSLLYVSMICVFHSKYAGFMV--PYFLRKFFSQNATIQKEDTLAI
                                            ypypviliaifqngwtlgnihcqisgflmglsv----igsvfnitaiainrycyichsl
                                                                    FIFYVNVIVIFFIEFIMCSANCAILLFINELELWLATWLGVFYCAKVASVRHPLFIWLKM
                                                                                                                  LESHLIIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKMAPL-DLLLSCLAVSRIFLQL
rydklyngrstwcylgltwiltiiaivpnffvgslgydprifsctfag--tvsssytitv 196
                                                                                            1997-132635/12
                                                                                                                                               Similarity
57; Conserv
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                                                                                                                                             7.8%;
ilarity 19.4%;
Conservative (
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172..19
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                                                                                                                                             Score 118; DB 18;
Pred. No. 1.2e-05;
4; Mismatches 119;
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        WPI; 1997-132635/12.
N-PSDB; T79065-6.
                                Jockers R,
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                                Marullo
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                                                                 95FR-0008947
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126..1
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108..1
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57..68
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor designated MEL-IAb, also known as Mel I-c(beta). The protein differs from previously known receptors by being 65 amino acids shorter and also differs throughout the sequence by 6 amino acids. The protein is encoded by 2 different alleles (T79065-6) which differ in the 3' untranslated region (both sequences encode the same protein), which is thought to affect the half-life of the mRNA. The coding sequence was isolated from cDNA derived from Xenopus skin RNA and amplified using the primers T79067-76. The nucleotide sequence encodes a 7 transmembrane receptor involved in cellular signalling. MEL-IAb has been shown to modulate intracellular cGMP, esp. inhibiting its accumulation induced by an inhibitor of phosphodiesterase, but unlike the MEL-IAb protein, it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequences W25926-7 represent novel allelic receptor MEL-1A proteins. This sequence is receptor designated MEL-1Ab, also known as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding functional melatonin receptor of Xenopus for screening for potential (ant)agonists useful for e.g. treating cardiovascular disease and cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cannot inhibit adenylyl cyclase activity.
                                                                                                                                Melatonin receptor; G-protein-coupled receptor; glycosylation; disulfide bond; ligand binding pocket; phosphorylation; cytochrome-c family heme binding site; melatonin receptor-agonist; melatonin receptor-antagonist; circadian rhythm disorder; jet-lag; day-night cycle disorder; ovulation; reproductive cycle; antibody; animal breeding; puberty; transgenic animal; drug screening.
                                                                                                                                                                                                                                                       High-affinity melatonin receptor
                                                                                                                                                                                                                                                                                         15-AUG-1996
                                                                                                                                                                                                                                                                                                                                                          R88409 standard; Protein; 420
                                                                                                  Xenopus laevis
                 Modified-site
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57; Conserv
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                                 /note= "Extracellular domain"
                                                                  Location/Qualifiers
 /note= "N-glycosylation site"
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19.4%;
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%; pred. No. 1.2e-05;
64; Mismatches 119;
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                                     06-JUN-1995;
17-JUN-1994;
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(MASS-) MASSACHUSETTS GEN HOSPITAL
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94US-0261857.
94US-0319887.
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57..68
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                                                                              95WO-US07360
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395
                                                                                                                                                                                                                                                /note= "Protein-kinase-C phosphorylation 328
                                                                                                                                                                                                                                                                          /note-
320
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                                                                                                                                                                                  "Protein-kinase-C phosphorylation
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Best Local S
Matches 57
                            Pheromone receptor; vomeronasal sensory neuron; social behaviour; maternal behaviour; reproductive behaviour; fertility;
                                                                                      Rat pheromone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  form of a ligand binding pocket. Phosphorylation sites in the encoding bnA may be used for isolation of sheep, mouse and human receptor sequences. Receptor fragments which interact with melatonin, or specific antibodies; may be used as receptor-agonists or receptor-antagonists. Agonists may be used in therapy of circadian rhythm disorders such as jet-lag or day-night cycle disorders, to control ovulation, or in alteration of reproductive cycles in seasonally breeding animals. Antagonists may be used to control the initiation or timing of puberty in humans. The receptor gene may also be expressed in a transgenic animal for use as a model system to screen agonists and antagonists.
                   hormone
                                                                                                                      26-AUG-1997
                                                                                                                                                         W19105
                                                                                                                                                                                         W19105 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coupled to guanine nucleotide binding proteins (G-proteins), and has 7 hydrophobic putative transmembrane domains. The N-terminus has an N-linked glycosylation site typical for G-protein-coupled receptors, and 2 Cys residues in the 1st 2 extracellular loops may form a stabilizing disulfide bond. Pro residues in transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding high affinity melatonin receptor one - used to identify receptor agonists or antagonists e.g. for regulating circadian rhythm disorders or reproductive cycles
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DB; T09947.
                   secretion
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57; Conservative
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                                                                                    receptor VN4
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19.4%; Pred. No. 1
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Rat pheromone receptors VNI, VN3, VN4, VN5, VN6, VN7 and VN2 (M19103-09) are members of a novel family of presumed 7-transmembrane domain receptors that are evolutionary independent of the odorant receptors of the main olfactory epithelium (MOE). Their amino acid sequences were deduced from cDNA clones (see also T69545-50, VN2 sequence not provided) obtd. by differential cloning, PCR and hybridisation from single vomeronasal sensory neurons (VSN). Individual neurons express different complements of the receptors. VN polypeptides can be expressed in host-vector systems for use in identifying modulators for control of maternal, reproductive and social behavior, to increase fertility, control permane against and to receive the receptors.
                                                                                                                                                                   Nucleic acid molecule encoding vertebrate pheromone receptor -useful to identify modulators for control of reproductive and social behaviour, fertility and hormone secretion
 hormone secretion and to
                                                                                                                                                Disclosure; Page 79-80; 123pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                         "the amino acid sequence deduced from the nucleotide sequence has a lysine residue between Met-263 and Phe-264"
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                                                                                                                                                                                                                                                                                                              Glucose transporter; GLUT-1; GLUT-2; chimeric transporter; diabetes; cancer; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                               W17836;
                                                                                                                                                                                                                                                                                                                                                                                                                     W17836 standard; Protein; 522
                                                                                                                                                                                                                                                                                                                                                Rat glucose transporter GLUT-2
                                                                                                                                                                                                                                                                                                                                                                       24-NOV-1997
                                                       Use of glucose transporter, GLUT-2 or GLUT-2 chimera(s) for cell-killing - used in negative and double selection protocols and screening methods, for cancer treatment and treatment of diabetes
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This polypeptide comprises rat glucose transporter GLUT-2. A claimed chimeric transporter comprises a contiguous amino acid
                                    Claim 137; Page 115-119; 169pp; English
                                                                                                                                        Clark SA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LYVSMICVFHSKYAGFMVPYFLRKFFSQNAT-----IQKEDTLAIQIFSFVAEFSVPLL 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             stscqsliylhrlsrgftlsaacllnvfwmitlsskkscl----tkfkhnsphhisgaf 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SANCAILLFINELE----LWLATWLGVFYCAKVASVRHPLFIWLKMRISKLVPWMILGSL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            car
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YFSHCMIKVFLSSLKFHIRRFIFLFFILVIGIYPSGHSLILILGNPKLKQNAKKFLLHSK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vreaffigl {\tt malssgylvaflwrhrkqaqhlhstglssksspeqratetill} {\tt msffvvl}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I---FLFAVL----LLIFSLGRHTROMRNT----VAGSRVPGRGAPISALLSILSFLIL
                                                                                                                1997-297737/27.
                                                                                                                                                               BETAGENE INC.
UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306
                                                                                                                                       Newgard CB,
                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                95US-0546934
                                                                                                                                                                                                                       96WO-US17327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.7%; Score 117.5; DB 18; 20.8%; Pred. No. 1.2e-05;
                                                                                                                                         Normington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                           Ğ
                                                                                                                                         Thigpen AE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence from human GLUT-1 (see W17835) operatively linked to a contiguous amino acid sequence from rat GLUT-2. The GLUT-1/GLUT-2 chimeric transporter confers glucose sensing capacity to a cell without rendering the cell subject to diabetta immune destruction. C and does not transport streptozotocin. The chimeric transporter comay be expressed in vivo by administration of a claimed chimeric polynucleotide (see T66495-96) for treatment of diabetes, or expressed in a host cell to prepare a recombinant cell that secretes insulin in response to glucose and which can be administered to a patient to treat diabetes. GLUT-2 can also be and on claimed methods of cell killing, such as negative selection cand double seletion protocols in vitro, in screening methods for cidentifying genes, promoters and substrates, and in cell killing in vivo, such as may be used in cancer treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                       RESULT 13
Y13352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 52
17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
                                                                                                  25-NOV-1997;
17-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                              Secreted protein; transmembrane protein; human; enterocolitis; 2011nger-Ellison syndrome; gastrointestinal ulceration; congenital microvillus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y13352 standard;
                                                                                                                                                                                                                                                                                                            Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of protein PRO228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    302 ivvalmlhlaqqfsgi--ngifyystsifqtagis-----qpvyatigvgainmifta 352
                                                                                                                                                        16-SEP-1998;
                                                                                                                                                                                           25-MAR-1999
                                                                                                                                                                                                                            W09914328-A2
                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                             anti-thrombotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        435 alaafsnwvcnfiialcfqyiadflgpyvfflfagvvlvftl 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 MRISKLVPWMILGSLLYVSMICVFHSKYAGFM-----VPYFL-RKFFSQNATIQKEDTL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 AIQIFS-----FVAEFSVPLLIFLFAVLLLIFSL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               385 lvlldkftwm----syvsmtaif--lfvsffeigpgpipwfmvaeffsqg---prptal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 LFIFYVNVIVIFFIEFIMCSANCAILLFINELELWLATWLGVFYCAKVASVRHPLFIWLK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 LIIYFLLAVIQELLGIFTNGI-----IVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vsvllvek-----vfmslg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                 97US-0066840.
97US-0059113.
97US-0059115.
97US-0059117.
97US-0059119.
                                                                                                                                                        98WO-US19330
                                                                                                                                                                                                                                                                                                 wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.7%; Score 117.5; DB 1
23.4%; Pred. No. 2.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            690
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                                                                                                                                                                                                                                                                                                   tissue
                                                                                                                                                                                                                                                                                                   repair.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          434
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11;

97US-0059121. 97US-0059122. 97US-0059184.

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The cDNA sequences are obtained from cDNA libraries, prepared from CC fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina. CC The encoded polypeptides have specific uses based on their homology to CC associated with the preservation and maintenance of gastrointestinal CC mucosa and the repair of acute and chronic mucosal lesions (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal CC ulceration and congenital microvillus atrophy), skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial CC cancers such as lung squamous cell carcinoma of the vulva and gliomas), CC potent effects on cell growth and development, diseases related to growth cor survival of nerve cells including Parkinson's disease, Alzheimer's CC disease, ALS, neuropathies or cancer pro265 can be used as for CC fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used as a target for anti-tumor drugs. PRO253 may be used in the treatment CC of Usher Syndrome or Atrophia areata; pRO269 can be used as an anti-tumor drugs. PRO269 can be used as an anti-tumor drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-OCT-1997;
29-OCT-1997;
29-OCT-1997;
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18-SEP-1997;
15-OCT-1997;
17-OCT-1997;
17-OCT-1997;
                                                                                                                                                                                                                                                                                                                              Claim 12; Fig 19; 320pp; English.
                                                                                                                                                                                                                                                                                              Y13344-403 represent secreted and transmembrane human
                                                                                                                                                                                                                                                                                                                                                              New isolated human genes and polypeptides used in, gastrointestinal ulceration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-NOV-1997
17-NOV-1997
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31-OCT-1997
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29-OCT-1997
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27-0CT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goddard A,
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97US-0066770.
97US-0066511.
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97US-0065846.
97US-0065693.
97US-0066120.
97US-0066364.
97US-0066772.
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97US-0063735.
97US-0063870.
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97US-0063732.
97US-0063738.
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97US-0063127.
97US-0063128.
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97US-0063435.
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RESULT
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8888
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Best Local
                      Modified-site
                                                                                            Modified-site
                                                                                                                                                                                                                                                                                  Inhibition; cancer; neoplasia; tumour; breast; ovary; renal; colorectal; uterus; prostate; lung; bladder; central nervous system; CNS; melanoma; leukaemia; pRO211; pRO228; pRO538; pRO172; pRO182;
 Modified-site
                                              Modified-site
                                                                     Modified-site
                                                                                                                     Modified-site
                                                                                                                                            Modified-site
                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                              Key
                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                  PRO288 Polypeptide
                                                                                                                                                                                                                                                                                                                                                            16-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                    Y83225
                                                                                                                                                                                                                                                                                                                                                                                                          Y83225 standard;
                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                           human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapeutic applications in wound healing and tissue repair; PRO317 can be used for treating problems of the kidney, uterus, endometrium, blood vessels, or related tissue, e.g. in the heart of genital tract.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 LFIWLKMRISKLVPWM-ILGSLLYVSMICVFHSKYAGFM-VPYFLRKFFSQNATIQKEDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----srkiqeeyyrlfknvpcc 685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IGIYPSGHSLILILGNPKLKQNAKKFLLHSKCC
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                                                                                                                                                                                                                                                                           88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    690
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                                                                                                                                                                                                                                                                                                                                                           (first
                                                                    /note=
52..58
                                                                                             /note= "|
4953..53
/note=
36..44
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64..68
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54..58
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50..56
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38..44
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21..25
                                                                                                                                                                                         /label = Signal_peptide
15..19
                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                          Protein; 690
                                                                                                                                                                                                                                                                                                                                                            entry)
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          "N-glycosylation site"
                                                                                                                              "N-myristoylation
                                "Casein kinase II phosphorylation site"
                                                       "N-myristoylation
                                                                                                      "N-myristoylation
                                                                                                                                                      "N-glycosylation site"
                                                                                                                                                                             "N-glycosylation
                                                                              "Glycosaminoglycan attachment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 117.5; DB 2
Pred. No. 3.3e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 114;
                                                                                                                                                                             site"
                                                        site"
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Modified-site
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94..98
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Bovine rhodopsin

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DB; Z93701.
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/note= "Tyrosine kinase phosports"
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59; Mismatches
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Bovine rhodopsin; 5HT1c receptor.

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                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                              Sequence codes for bovine rhodopsin. See also P90549-P90554, P92111 and N90955.
                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 11; 84pp; English.
                                                                                                                                                                                                                                                                                                                                      DNA encoding serotonin 5HTlc receptor - used for producing protein, antibodies and probes for studying receptor binding and screening drugs.
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167 QKEDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTROMRNTVAGSRVPGRGAPISA 226
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                                  153 aimgvaftwv-malacaap-plvgwsryipegmgc---scgidyytph--------
                                                       113 PL----FIWLKMRISKLVPWMILGSLLYV--SMICVFHSKYAGFMVPYFLRKFFSQNATI 166
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                                                                                                           65 VNVIVIFFIEFIMCSANCAILLFI----NELELW----LATWLGVFYCAKVASVR----H 112
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/label= VII
/note= "transmembrane domain.
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/label= VI
/note= "transmembrane domain."
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note= "transmembrane domain."
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                                                                                 227 LLSILSFLILYESHCMIKVFLSSLKFHIRRFIFL----FFILVIGIYPSGHSLILILGNP 282
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